

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 01:06:09 ; Search time 1066 seconds  
(without alignments)  
9784.140 Million cell updates/sec

Title: US-10-037-591a-1

Perfect score: 644

Sequence: 1 ctcaagtcactcctctaaataa.....ggcccggtgtgaggctag 644

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Capext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_estli:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_man:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	296.4	46.0	524	9 AI430337	AI430337 mf68b10.y
2	249.6	38.8	420	14 W88186	W88186 mf68b10.r1
3	229	35.6	553	13 BM540145	BM540145 hb18f07.g
4	145.4	22.6	344	12 BG609875	BG609875 324181.MA
5	96.6	15.0	480	13 BM124559	BM124559 L0541G02-
6	96.6	15.0	549	14 BQ554452	BQ554452 H4028C03-

C 7	47.4	7.4	925	17	CNS0091P	AL053013 Drosophil
C 8	47	7.3	997	17	CNS006DN	AL065132 Drosophil
C 9	43.8	6.8	868	12	BG821981	BG821981 602726077
C 10	43.2	6.7	925	17	CNS0091P	AL053013 Drosophil
C 11	43	6.6	568	14	BQ574994	BQ574994 UT-H-E21-
C 12	42.8	6.6	440	14	BQ779177	BQ779177 946117E05
C 13	42.4	6.6	839	17	CNS004NB	AL054280 Drosophil
C 14	42.2	6.6	460	10	BE357122	BE357122 DGL-146.B
C 15	42.2	6.6	486	9	AI388531	AI388531 GH19472.5
C 16	42.2	6.6	586	10	BE357121	BE357121 DGL-146.B
C 17	42.2	6.6	588	13	BM055698	BM055698 id85H04.x
C 18	42.2	6.6	633	13	BM330143	BM330143 PIC1 47.F
C 19	42.2	6.6	652	10	BE362682	BE362682 DGL-88.H0
C 20	41.6	6.5	441	9	AI064196	AI064196 GH04480.5
C 21	41.4	6.4	373	9	AI867949	AI867949 W890B08.x
C 22	41.4	6.4	396	9	AA680405	AA680405 z138H02.S
C 23	41.4	6.4	405	9	AI375735	AI375735 ta64C02.x
C 24	41.4	6.4	590	12	BF510968	BF510968 UT-H-B14-
C 25	41.4	6.4	629	14	BM826445	BM826445 K-EST0098
C 26	41.2	6.4	463	13	BM381881	BM381881 MEST541-D
C 27	41.2	6.4	488	9	AI854942	AI854942 605094E01
C 28	41.2	6.4	527	10	AW787570	AW787570 945011B07
C 29	41.2	6.4	540	10	AW927918	AW927918 945011B07
C 30	41.2	6.4	556	10	AW787571	AW787571 945011B07
C 31	41.2	6.4	567	10	BE129743	BE129743 946003H07
C 32	41.2	6.4	567	14	BQ280219	BQ280219 1091036B1
C 33	41.2	6.4	583	9	AI833725	AI833725 605094E01
C 34	41.2	6.4	584	14	BQ279494	BQ279494 1091036B1
C 35	41.2	6.4	586	10	BE511474	BE511474 946061B04
C 36	41.2	6.4	609	13	BM381419	BM381419 MEST534-E
C 37	41.2	6.4	615	10	AW424676	AW424676 707058E02
C 38	41	6.4	483	9	AI388053	AI388053 GH18791.5
C 39	40.8	6.3	1063	17	CNS07A2Y	AL436064 T3 end of
C 40	40.6	6.3	425	13	BI396114	BI396114 949044E02
C 41	40.6	6.3	441	13	BM382130	BM382130 MEST545-A
C 42	40.6	6.3	468	12	BF150243	BF150243 uy83e02.Y
C 43	40.6	6.3	497	13	BI388823	BI388823 949046B01
C 44	40.6	6.3	553	9	AI323984	AI323984 mb22a01.x
C 45	40.6	6.3	602	13	BM053185	BM053185 id66606.x

## ALIGNMENTS

RESULT 1  
AI430337  
LOCUS  
DEFINITION  
mf68b10.y1 Soares mouse embryo NBME13.5 14.5 Mus musculus CDNA  
clone IMAGE:419419 5', mRNA sequence.  
AI430337  
VERSION  
AI430337.1 GI:4276173  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 524)  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person  
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuck, R., Ritter  
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
This read is a RESEQUENCE of a previously sequenced mouse clone





Qy	186	ATGCTATGTGGAAACCCACAC-----	-CTACAGCACCATTGGCCC	221	
Dd	277	ATGGCCATGTGGAAACCCACAC	CTCAATTTTTCGGATCCCGAAGGACTGCACCCCACTGGCCT	336	
Qy	222	AGCTGCTGCCCCAGCAAAGGGCAGGACACCTCTGTAGGAGCTGCTGAGGTGGAGCACTGTG	281		
Dd	337	AACCTGCTGTCCCAAGCAAAGGCAAGGAGGACCCCACTCATGAGTGGCTGAAGCGGAGCACTGTG	396		
Qy	282	CCTGTGCTCCCCCTAGAGCCTGTCTAGGCGCCCAACCGCCACCCAGACTCCTGTSTAGGCGCCAGT	341		
Dd	397	CTCAAGTTCCCGGAGAGACCACTACGCTCACCCACCCAGAATCTCTGCAAAAGCCAGT	456		
Qy	342	GAGATGAGGACCCCTCAACAGCAGGCGCCATCTCCCCCTTGAGATATGAGTTGGACAGAGAC	401		
Dd	457	GAGACGAGGACCGCTCAACAGCAGGCTATCTATCTCCCTCGAAAATATGAGTTGGACAGGAC	516		
Qy	402	TTGAACCGCGTCCCGCAGGACCTGTACCACGCGCCGTT	438		
Dd	517	TTGACCGCGTCCCGCAGGACCTGTACCACGCGCCGTT	553		
RESULT	4				
LOCUS	BG609875	344 bp mRNA linear	EST 17-APR-		
DEFINITION	324181 MARC lPIG Sus scrofa cDNA 5', mRNA sequence.				
ACCESSION	BG609875				
VERSION	BG609875.1 GI:13659854				
KEYWORDS	EST.				
SOURCE	pig.				
ORGANISM	Sus scrofa				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W. and Keele,J.W. Design and use of two pooled tissue normalized cDNA libraries f EST discovery in swine Unpublished (2000) Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the "minscor and -mismatch 12 options. PCR Primers FORWARD: AGGAACAAGCTATGACCAT BACKWARD: GTTTCCTCAGTCACGCG Plate: 100 row: G column: 12 Seq primer: ATTTAGCTGACACTATAG. Location/Qualifiers 1..344 /organism="Sus scrofa" /db_xref="taxon:9823" /clone_lib="MARC lPIG" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from day 11, 13, 15, 21, and 30 embryos."				
BASE COUNT	64 a	128 c	86 g	56 t	
ORIGIN					
Query Match	22.6%	Score 145.4;	DB 12;	Length 344;	
Best Local Similarity	86.1%;	Pred. No. 1.2e-24;			
Matches 161;	Conservative	0;	Mismatches 26;	Indels 0;	Gaps
Qy	389	GTGTGGACAGACTTGAACCGCTCCCCAGAGCACTGTACACAGCCCGCTTGCCTGTGCCCC	448		
Dd	158	GTGTGGACAGACTTGAACCGCTCCCCAGAGCACTGTGTACACGCTTGTGCTGTGCTGTGCTG	217		

```

QY 449 GCACTGCGCTACAGACAGGCTCCACATGGACGCCCGGGCAACTCGAGCTGCT 508
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 ACATGCTGACGCTCGGACGGGTTCCACATGATCCCTGGGTAACTCAGAGTGT 277
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 509 CTACACAAACAGACTGCTTCTACCGGGGGCCATGCCATGCCGAGAGGACACACAA 568
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 278 GTACACAAACAGACGCTTCTTACCGGGGGCCGTCCTGGACAGAGGGGCCCATGA 337
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 569 GGGCTAC 575
      |||||
Db 338 TAGCTAC 344

RESULT 5
LOCUS BM124559 480 bp mRNA linear EST 01-FEB-2002
DEFINITION L0541G02-3 NIA Mouse Newborn Heart cDNA Library Mus musculus cDNA
ACCESSION BM124559
VERSION BM124559
KEYWORDS BM124559.1 GI:17108327
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Pantano, S., Lim, M.K.
and Ko, M.S.H.
TITLE Systematic Analyses of NIA Mouse Newborn Heart cDNA Library
JOURNAL Unpublished (2001)
COMMENT Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: L0541 row: G column: 02
Seq primer: -21M13 Forward
High quality sequence stop: 480
POLYA=Yes.

FEATURES             Location/Qualifiers
     source           1..480
     /organism="Mus musculus"
     /strain="C57BL/6J"
     /db_xref="niaEST:L0541G02-3"
     /db_xref="taxon:10090"
     /clone="L0541G02"
     /clone_lib="NIA Mouse Newborn Heart cDNA Library"
     /tissue_type="Newborn Heart"
     /dev_stage="Newborn"
     /lab_host="DH10B"
     /note="Organ: heart; Vector: pSPORT1 (Invitrogen); Site_1:
SalI; Site_2: NotI; Mouse cDNA project by the Laboratory
of Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer (Invitrogen, 5'-
pGACTAGTCTCAGATCGGAGCGCGCCCTTTTCTTTT-3') from
24.9 microgram of total RNA, treated with T4 DNA
polymerase, and purified by ethanol-precipitation. The
cDNAs were ligated to Lone-linker LL-Sal3 (Ref.
Development 127:1737-1749 (2000) [PMID: 10725249]),
purified by phenol/chloroform, and separated from free
linkers by Centricon 100. Then, the cDNAs were digested
with SalI and NotI enzymes, and cloned into SalI and NotI
site of pSPORT1 plasmid vector. The DH10B E. coli host was
transformed with ligation mixture by the chemical method.
The average insert size is about 1.8 kb. The library was
constructed by Yulan Piao (NIA)."
```

BASE COUNT 112 a 99 c 143 g 126 t

Query Match

15.0%; Score 96.6; DB 13; Length 480;

```

Best Local Similarity 79.4%; Pred. No. 6.6e-13;
Matches 139; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

QY 1 CTCAACTCACTCCCT-AAAAAGACAGTGGAAATAAATTTGAATAAACAACAGGCTTGC 59
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26 CTCAGTCACTCCCTCTAAAGATAGTGGAAATAAATTTGAATAAACAACAGGTTGC 85
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 60 TGAATAAATAATCAGACGCTTAACTGCTCCAGTCCAGTCCAGTCCAGGCGCTGTCA 119
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 86 TGAATAAATAAACGAGCACCTCAGCTGCTCCAGTCCAGCT-CTCTCAGAAGGCGTGTCA 144
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 120 CTCAGTGGCCCACTTGTGACTGAGTGGCAGTCCCGCAGCATGTACCAGGTGGTTG 174
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 145 GGCAGGGGTAGTACCTGTGACTGGTGAGCAGTGTCCGCGCATGTACCAGGTGAGTG 199
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
LOCUS BQ554452 549 bp mRNA linear EST 20-JUN-2002
DEFINITION H4028C03-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
ACCESSION BQ554452
VERSION BQ554452
KEYWORDS BQ554452.1 GI:21455340
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin
, P.R., Stagg, C.A., Bassey, U., Alba, K., Hamatani, T., Kargul, G.J.,
Luo, A.G. and Ko, M.S.H.
TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse
JOURNAL cDNA clone set
COMMENT Unpublished (2002)
Other ESTs: H4028C03-5
Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7.4k.html for details.
Plate: H4028 row: C column: 03
Seq primer: -21M13 Forward
High quality sequence stop: 549
POLYA=Yes.

FEATURES             Location/Qualifiers
     source           1..549
     /organism="Mus musculus"
     /strain="C57BL/6"
     /db_xref="niaEST:H4028C03-3"
     /db_xref="taxon:10090"
     /clone="H4028C03"
     /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
     /sex="mixed"
     /dev_stage="mixed"
     /lab_host="DH10B"
     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."
```

BASE COUNT 129 a 121 c 164 g 135 t

ORIGIN

Query Match 15.0%; Score 96.6; DB 14; Length 549;

Best Local Similarity 79.4%; Pred. No. 6.8e-13;  
Matches 139; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

QY 1 CTCAACTCACTCCCT-AAAAAGACAGTGGAAATAAATTTGAATAAACAACAGGCTTGC 59

Db 26 CTCAGTCACTCCCTCTAAAGATAGTGGAAATAAATTTGAATAAACAACAGGTTGC 85

QY 60 TGAATAAATAATCAGGACTCTAACCTGCTCCAGTCCAGCTTCCAGGCGCTGTCA 119

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||||| 86 TGAATAAACAGGACACCTGCTGCTCCAGTCACGCT-CTCTCAGAAGGCGCTGTCA 144
||||| 120 GTACAGTCCCGACCTGTGACTGAGTGTGCTGAGTGCAGCCAGTGTACCAAGGTGTTG 174
||||| 145 GGCAGGGGTAGTACTGCTGAGTGTGAGCAGTGTCCGCACTGTACCAAGGTGAGTG 199

RESULT 7
CNS0091P/c      925 bp      DNA      linear      GSS 03-JUN-1999
LOCUS           Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION      BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                  fly), genomic survey sequence.
ACCESSION       AL053013
VERSION         AL053013.1 GI:4934461
KEYWORDS        GSS.
SOURCE          Drosophila melanogaster.
ORGANISM        Drosophila melanogaster.
                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Ephydroidea; Drosophilidae; Drosophila.
REFERENCE       1 (bases 1 to 925)
AUTHORS         Genoscope.
TITLE           Direct Submission
JOURNAL         Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT         Determination of this BAC-end sequence was carried out as part of a
                collaboration with the Berkeley Drosophila Genome Project (BDGP).
                The BDGP is constructing a physical map of the Drosophila
                melanogaster genome using these BACs. For further information
                please see http://www.fruitfly.org The BDGP Drosophila
                melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                Aaron Mammosier in Pieter de Jong's laboratory in the Department of
                Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                NY. The library is named RPCI-98 and was constructed by partial
                EcoRI digestion of Drosophila DNA provided by the BDGP from the
                isogenic strain y2; cn bw sp, the same strain used for the BDGP's
                pl and EST libraries. A more detailed description of the library
                and how to order individual BAC clones, the entire library, or
                filters for hybridization from the BACPAC Resource Center can be
                found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES         Location/Qualifiers
                source             1..925
                                /organism="Drosophila melanogaster"
                                /db_xref="taxon:7227"
                                /clone_lib="RPCI-98"
                                /note="end : TET3"

BASE COUNT      120 a      61 c      172 t      511 others
ORIGIN

Query Match     7.4%; Score 47.4; DB 17; Length 925;
Best Local Similarity 11.1%; Pred. No. 0.49;
Matches 37; Conservative 160; Mismatches 136; Indels 0; Gaps 0;

QY 227 CTCGCCAGAAAGGCGGACACCTCTGAGGAGCTCTGAGTGGGAGCAGTGTGCTGT 286
Db 924 SBSCSCSCSCSBSCTSSNSTSSNSBSCSSBSSTSSSSTSSSBSSTSSSBSSTSS 865
QY 287 GCCTCCCTAGAGCTGTAGGCGCCACCGCCACCGAGCTCTGTAGGCGCAGTGA 346
Db 864 SGTSSACVKNASSCGCCCGCAGBACCMCSSTSSSCGASARGVKVRASGAGRGGSG 805
QY 347 TGGACCCCTCAACAGCAGGCGCCATCTCCCTCGGAGATATAGTTGACAGAGACTTGA 406
Db 804 GASASHSSSACBSSTSCSASCSWSSSSSSASSRSRSGGAGGSGASSRSSSSSSA 745
QY 407 CCGGCTCCCGAGGAGCTGTACACGCGCCGTTGCTGTGCGCCGAGCTGCTCAGCTTACA 466
Db 744 SAGSVYSSASSSSSSSSSVSCSVASSMSCSBSBSSTSSASASSSSSSSSASCSCCCT 685
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QY 467 GACAGGCTCCCATGACGACCCCGGGGCAACTGGAGCTGCTCTACCAACACGAGCTGT 526
Db 684 SWSCTSTASMSAARSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 625
QY 527 CTTCTACCGCGGCGCATGCGCATGCGGCGAGAGGG 559
Db 624 MSSGGGSGSVASSGMSSSSVSSSGRSGSGGG 592

RESULT 8
CNS006DM/c      997 bp      DNA      linear      GSS 03-JUN-1999
LOCUS           Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION      BACR13C17 of RPCI-98 library from Drosophila melanogaster (fruit
                  fly), genomic survey sequence.
ACCESSION       AL065132
VERSION         AL065132.1 GI:4944302
KEYWORDS        GSS.
SOURCE          Drosophila melanogaster.
ORGANISM        Drosophila melanogaster.
                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Ephydroidea; Drosophilidae; Drosophila.
REFERENCE       1 (bases 1 to 997)
AUTHORS         Genoscope.
TITLE           Direct Submission
JOURNAL         Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT         Determination of this BAC-end sequence was carried out as part of a
                collaboration with the Berkeley Drosophila Genome Project (BDGP).
                The BDGP is constructing a physical map of the Drosophila
                melanogaster genome using these BACs. For further information
                please see http://www.fruitfly.org The BDGP Drosophila
                melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                Aaron Mammosier in Pieter de Jong's laboratory in the Department of
                Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                NY. The library is named RPCI-98 and was constructed by partial
                EcoRI digestion of Drosophila DNA provided by the BDGP from the
                isogenic strain y2; cn bw sp, the same strain used for the BDGP's
                pl and EST libraries. A more detailed description of the library
                and how to order individual BAC clones, the entire library, or
                filters for hybridization from the BACPAC Resource Center can be
                found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES         Location/Qualifiers
                source             1..997
                                /organism="Drosophila melanogaster"
                                /db_xref="taxon:7227"
                                /clone_lib="RPCI-98"
                                /note="end : TET3"

BASE COUNT      76 a      145 c      120 g      177 t      479 others
ORIGIN

Query Match     7.3%; Score 47; DB 17; Length 997;
Best Local Similarity 15.5%; Pred. No. 0.62;
Matches 54; Conservative 157; Mismatches 137; Indels 0; Gaps 0;

QY 268 GGTGAGAGCAGTGTGCTGTGCTGCTCCCTAGAGCCTGTAGGCCCAACGCCACAGT 327
Db 898 KGKDGWGYTKMKRKBVBABSKBTSCNGBSGBKSCSMBKSKSYGKGVYCGGSGS 839
QY 328 CCTGTAGGCCAGTGAAGATGAGCCCTCAACAGCAGGCGCCATCTCCCTCGGAGATATG 387
Db 838 MVKCKGKGGCGAGGKGGGKGGVVGKSGCGCGGSCSVMSCSKBFGCMKSGCKC 779
QY 388 AGTTGGACAGAGACTTGAACCGGCTCCCGCCAGGACTGTACACGCGCCGTGCTGTGCC 447
Db 778 VGGGGGGMTAANAANRABAKBKBBSYBMBMHKICGYTCMMWYTGKSTCSMYKSBHG 719
QY 448 CGCACTGCGTCACTACAGCAGCTCCCATGACATGACCCCGGGGCAACTCGGAGCTGC 507
Db 718 SBGTTGKSGSMABBBGBDBKSCCRMAAYGKKGKKGKBYNKGKMKSKVVBGTGVBKG 659
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LOCUS BQ779177 440 bp mRNA linear EST 26-JUL-2002  
 DEFINITION 946117E05.xl 946 - tassell primordium prepared by Schmidt lab Zea  
 may's cDNA, mRNA sequence.  
 ACCESSION BQ779177  
 VERSION BQ779177.1 GI:21987649  
 KEYWORDS EST.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 1. (bases 1 to 440)  
 Walbot, V.  
 Maize ESTs from various cDNA libraries sequenced at Stanford  
 University  
 UNPUBLISHED (1999)  
 CONTACT: Walbot V  
 DEPARTMENT OF Biological Sciences  
 STANFORD UNIVERSITY  
 855 CALIFORNIA AVE, PALO ALTO, CA 94304, USA  
 TEL: 650 723 2227  
 FAX: 650 725 8221  
 EMAIL: walbot@stanford.edu  
 PLATE: 946117 row: E column: 05.  
 Location/Qualifiers  
 1. 440  
 /organism="Zea mays"  
 /cultivar="OH43"  
 /db\_xref="taxon:4577"  
 FEATURES source

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/clone_lib=946 - tassell primordium prepared by Schmidt
lab"
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inflorescence development"
/lab_host="XLOLA"
/note="Organ: tassels; Vector: HybrizAP; Site_1: EcoRI;
Site_2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybrizAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."
BASE COUNT 107 a 132 C 108 g 93 t
ORIGIN

Query Match 6.6%; Score 42.8; DB 14; Length 440;
Best Local Similarity 47.7%; Pred. No. 5;
Matches 125; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

QY 377 CTGGAGATATGAGTTGACACAGACATTGACCGGCTCCCCCAGGACCTGTACACAGCCCG 436
||||| + ||||| + ||||| + ||||| + ||||| + ||||| + ||||| +
Db 398 CTGGATCGCGGCTGGGGACATCTGCTCTCGCGGCTCCGGGACTTACGAGGACGACAGGC 339
||||| + ||||| + ||||| + ||||| + ||||| + ||||| + ||||| +
QY 437 TTGCCTGTGCCCGCACCTGCGCTCAGCGCTACAGACAGGCTCCCATATGGACCCCGGGGCAA 496
||||| + ||||| + ||||| + ||||| + ||||| + ||||| + ||||| +
Db 338 CGAGCTTATCTCAAGTACATGACGACGAGGCGCGCTGCTCAAGGCTTACGGGGAGCT 279

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Db	278	TCTGTACACGCTCAGGCTCAACGAGGCGCTCGACGTCGATGGGCGCCGAGGAAGCGGAGGA	219
Qy	557	GGGCACCACCAAGGGCTACTGCTGGAGCGCAGCGCTGTACCGTCTTTCTTAGCTTCTGT	616
Db	218	GGGCGAGCGCTACTCAGCTTCGAGGACGAGGACATCGACAAGATTTAAGAAATCTCTTC	159
Qy	617	GTGTGTGCGGGCCCGTGTGATG	638
Db	158	CTGCTTACGGCTACCTGTATTG	137

RESULT 13

LOCUS	CNS004NB	839 bp	DNA			
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC #					
	BACR10E16 of RPCI-98 library from Drosophila melanogaster (fruit					
	fly) (GSS 03-JUN-1999)					



REFERENCE 1 (bases 1 to 486)  
AUTHORS Harvey D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,  
Lewis, S., and Rubin, G.M.  
TITLE BDGP/HMI Drosophila EST Project  
JOURNAL Unpublished (2001)  
COMMENT Contact: Stapleton, M.  
BDGP

Lawrence Berkeley National Lab  
One Cyclotron Rd, Berkeley, CA 94720, USA  
Fax: 510 486 6798  
Email: <http://www.fruitfly.org/EST>, [est@fruitfly.berkeley.edu](mailto:est@fruitfly.berkeley.edu)  
Plate: 194 row: F column: 12  
High quality sequence stop: 343.

FEATURES Location/Qualifiers  
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1..486  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone="GH19472"  
/clone\_lib="GH Drosophila melanogaster head pot2"  
/sex="male and female"  
/dev\_stage="adult"  
/lab\_host="DH5 - alpha"  
/note="Organ: head; Vector: pot2; Site\_1: EcoRI; Site\_2:  
xhoI; Sized fractionated cDNAs were directly ligated into  
pot2. plasmid cDNA library."  
BASE COUNT 64 a 97 c 205 g 119 t 1 others  
ORIGIN

Query Match 6.6%; Score 42.2; DB 9; Length 486;  
Best Local Similarity 50.0%; Pred. NO. 8;  
Matches 104; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
QY 394 ACAGAGACTGTGACCGGCTCCCGGAGGCTGTACACGCGCGCTGTGCTGCGCGGACT 453  
DB 452 ACCGAGGATTCGCGGACCTCTCCGGAATATCCACCTGATCCAAATCCAGGCGGTCACC 393  
QY 454 GCCTCAGCCTACAGACAGGCTCCGACATGGACCCCGGGGCAACTCGGAGCTGCTTACC 513  
DB 392 GATTCCTCCACCGAATGACCACTGATCCGGAATCCGGGACCGCCACNGAATCGGCTCC 333  
QY 514 ACAACGAGACTGTCTTCTTACCGGCGGCGATGCCATGGCGAGAGGGCACCCACAAGGGCT 573  
DB 332 ACCTCCAGAAATGACCTCCGCGCGGAGATCACTCCACCGCCAGCATGGCCACCTGCGAAGGG 273  
QY 574 ACTGCTGGAGCGCAGGCTGTACCGTGT 501  
-DB 272 ACCTCTCCGACACACCGCGGCTCCAAAGT 245

Search completed: May 12, 2003, 01:55:16  
Job time : 1074 secs



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 12, 2003, 01:59:44 ; Search time 163 seconds  
(without alignments)  
2224.366 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MTQVAFVLAAMVMTGTHYSHW.....ERRLYRVSLACVCRVRVNG 161

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi  
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-NO\_XLPXY -NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*\*  
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	910	100.0	504	21	AAA58986	cDNA encoding a hu
2	910	100.0	504	21	AAA59158	cDNA encoding a hu
3	910	100.0	504	24	ABA02393	Human interleukin
4	910	100.0	644	24	AAD28771	Human interleukin-
5	910	100.0	644	24	ABA03213	Human IL-17 recept
6	898	98.7	1320	22	AAS09511	Human cDNA encodin
7	898	98.7	1320	22	AAC85969	Native sequence of
8	898	98.7	1320	22	AAF92135	Human PRO10272 cDN
9	834	91.6	1355	23	AAS35559	DNA encoding novel
10	709	77.9	985	21	AAA58988	cDNA encoding a mu
11	709	77.9	985	21	AAA59160	cDNA encoding a mu
12	709	77.9	985	24	ABA02394	Murine interleukin
13	709	77.9	1013	24	AAD28772	Mouse Interleukin-
14	693	76.2	1496	24	AAD28773	Mouse non-secreted
15	493	54.2	620	21	AAA58987	cDNA encoding a mu
16	493	54.2	620	21	AAA59159	cDNA encoding a mu
17	167	18.4	591	21	AAA09153	Human interleukin-
18	167	18.4	591	24	AAD38083	Human LP-48 gene.
19	167	18.4	1047	21	AAA96338	cDNA encoding a no
20	167	18.4	1047	21	AZ29728	Human Interleukin
21	167	18.4	1047	22	AAZ46148	Human DNA encoding
22	167	18.4	1047	22	AAS09510	Human cDNA encodin
23	167	18.4	1067	21	AZ36836	Nucleotide sequenc
24	167	18.4	1067	23	AAI67878	Human interleukin
25	167	18.4	1107	21	AAA58991	cDNA encoding a hu
26	167	18.4	1107	21	AAA59149	cDNA encoding a hu
27	167	18.4	1177	22	AAD15291	Human interleukin
28	136.5	13.9	1385	21	AAA58983	cDNA encoding a hu
29	136.5	13.9	1385	21	AAA59155	cDNA encoding a hu
30	136.5	13.9	1819	21	AAZ52195	Human transforming
31	136.5	13.9	2361	21	AAZ52201	Human transforming
32	125.5	13.8	540	20	AAZ89401	Human interleukin-
33	125.5	13.8	543	21	AAA58980	cDNA encoding a hu
34	125.5	13.8	543	21	AAA59152	cDNA encoding a hu
35	125.5	13.8	687	20	AAC34282	Human PRO1031 nucl
36	125.5	13.8	687	21	AAZ78577	Human PRO1031 (UNQ
37	125.5	13.8	687	21	AAZ75694	cDNA clone DNA5929
38	125.5	13.8	687	21	AAC58608	Human PRO1031 prot
39	125.5	13.8	687	21	AZ29727	Human Interleukin
40	125.5	13.8	687	22	AAS09509	Human cDNA encodin
41	125.5	13.8	687	22	AAS21466	Human cDNA sequenc
42	125.5	13.8	687	22	AAC91479	Human PRO1031 cDNA
43	125.5	13.8	687	22	AAC88961	Human PRO1031 codi
44	125.5	13.8	689	21	AAA95780	Human immune syste
45	125.5	13.8	704	22	AAH79255	Human cell factor-

ALIGNMENTS

RESULT 1

AAA58986

ID AAA58986 standard; cDNA; 504 BP.

XX

AC AAA58986;

XX

DT 07-NOV-2000 (first entry)

XX cDNA encoding a human interleukin (IL) 174 polypeptide.

DE Interleukin; IL-17; CTIA-8; IL-170; IL-172; IL-173; IL-174; IL-176;

KW IL-177; IL-171; cell proliferation; cancer; ss.

XX Homo sapiens.

OS

XX

PH Key Location/Qualifiers

FT CDS 19..504

FT /\*tag= a

[illegible]

Score: 910.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0

US-10-037-591A-2 (1-161) x ABA02393 (1-504)

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QY 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrp 20
DB 19 ATGTACCAGGTGGTTCATTCTGGCAATGCTCATGGAAACCCACCTACAGCCACTGG 78
QY 21 ProSerCysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThr 40
DB 79 CCCAGCTGCTGCCCCAGCAAAAGGCGAGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT 138
QY 41 ValProValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAla 60
DB 139 GTGCCTGTGCTCCCTAGAGCCTGCTAGGCCCAACCGCCACCCAGAGTCTGTAGGGCC 198
QY 61 SerGluAspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArg 80
DB 199 AGTGAAGATGGACCCCTCAACAGCAGGCGCATCTCCCTCTGGAGATATGAGTTGGACAGA 258
QY 81 AspLeuAsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysVal 100
DB 259 GACTTGAACGGCTCCGCCAGGACCTGTACACAGCCGCTTGCCTGTGCCGCACTGGCTC 318
QY 101 SerLeuGlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsn 120
DB 319 AGCCTACAGACAGGCTCCACATGACGCCCGGGGCACTCGGAGCTGCTCTACCCACAC 378
QY 121 GlnThrValPheTyrArgTyrProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140
DB 379 CAGACTGCTCTTACCGCGGCCATGCTCCAGAGAGGCGCCACCCAGAGGCTGCTGATG 438
QY 141 LeuGluArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMet 160
DB 439 CTGGAGCGCAGGCTGTACCGGTTCCTTCTAGCTTGTGTGTGTGTGTGTGTGTGTGTGT 498
QY 161 Gly 161
DB 499 GGC 501

RESULT 3
ID ABA02393 standard; DNA; 504 BP.
XX AC ABA02393;
XX DT 26-FEB-2002 (first entry)
XX DE Human interleukin 174 (IL-174)-encoding DNA.
XX KW Human; interleukin 174; IL-174; cytokine; Th2 response;
KW innate immune response; inflammation; gut cell growth;
KW extramedullary haematopoiesis; antibody response; granuloma formation;
KW autoimmune condition; multiple sclerosis; systemic lupus erythematosus;
KW rheumatoid arthritis; diabetes; psoriasis; infectious agent;
KW inflammatory condition; Crohn's disease; ulcerative colitis;
KW pancreaticitis; hepatitis; allergy; Th2-mediated condition;
KW systemic anaphylactic response; skin hypersensitivity response;
KW dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator;
KW antiinflammatory; antiarthritic; antidiabetic; antifungal;
KW dermatological; neuroprotective; anti-allergic; agonist; antagonist; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
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FT FT /*tag= a
FT FT /product= "Human IL-174"
FT FT sig_peptide 19..66
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FT mat\_peptide /\*tag= b  
FT 67..501 /\*tag= c  
FT /\*product= "Mature human IL-174"  
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PN WO200179288-A2.

XX 25-OCT-2001.

XX 17-APR-2001; 2001WO-US12493.

XX 18-APR-2000; 2000US-198488P.

XX (SCHE ) SCHERING CORP.

PI Hurst SD, Zurawski SM, Rennick DM;

XX WPI; 2002-034343/04.

XX P-PSDB; AAM52691.

XX Administering an interleukin 174 agonist or antagonist to a mammal  
PT regulates various immune and inflammatory responses and is useful to  
PT treat for example autoimmune diseases, allergies or response to an  
PT infection

XX Disclosure; Page 26-27; 29pp; English.

XX The invention relates to methods of directing an immune response in a  
CC mammal by the administration of an agonist or antagonist of the cytokine  
CC interleukin 174 (IL-174). Administration of an IL-174 agonist directs the  
CC immune response towards a Th2 response, stimulates an innate immune  
CC response, augments the inflammatory response from epithelial or  
CC fibroblast cells, induces gut cell growth, promotes extramedullary  
CC haematopoiesis, or augments an antibody response in serum and faecal  
CC material, while administration of an IL-174 antagonist directs the immune  
CC response away from a Th2 type response, and prevents inflammation or  
CC granuloma formation. IL-174 agonists may be used to treat autoimmune  
CC conditions (particularly multiple sclerosis, systemic lupus  
CC erythematosus, rheumatoid arthritis, diabetes or psoriasis), a response  
CC to an infectious agent, or inflammatory conditions such as Crohn's  
CC disease, ulcerative colitis, pancreatitis, or hepatitis. IL-174  
CC antagonists may be used to treat inflammatory, allergic or Th2-mediated  
CC conditions (e.g., systemic anaphylactic response, skin hypersensitivity  
CC response, dermatitis, asthma, fibrosis, or eosinophilic gastritis). The  
CC present sequence represents DNA encoding human IL-174.

XX SQ. Sequence 504 BP; 98 A; 165 C; 148 G; 93 T; 0 other;

Alignment Scores:

Pred. No.: 3 01e-74 Length: 504  
Score: 910.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0

US-10-037-591A-2 (1-161) x ABA02393 (1-504)

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QY 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrp 20
DB 19 ATGTACCAGGTGGTTCATTCTGGCAATGCTCATGGAAACCCACCTACAGCCACTGG 78
QY 21 ProSerCysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThr 40
DB 79 CCCAGCTGCTGCCCCAGCAAAAGGCGAGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT 138
QY 41 ValProValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAla 60
DB 139 GTGCCTGTGCTCCCTAGAGCCTGCTAGGCCCAACCGCCACCCAGAGTCTGTAGGGCC 198
QY 61 SerGluAspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArg 80
DB 199 AGTGAAGATGGACCCCTCAACAGCAGGCGCATCTCCCTCTGGAGATATGAGTTGGACAGA 258
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QY 81 AspLeuAsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysVal 100  
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 Db 259 GACTGAACCGCGCTCCCGCAGGACCTGTACACCGCGTTCCTGTGCGCGCTGGGTC 318  
 QY 101 SerLeuGlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsn 120  
 |||  
 Db 319 AGCCTACAGACAGCGCTCCACATGGACCGCGGCAACTCGGAGCTGCTCTACCAAC 378  
 QY 121 GlnThrValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140  
 |||  
 Db 379 CAGACGTCTTCTACCGCGCGCGCATGCGTGGAGAGGCGACCCACAGGGCTACTGC 438  
 QY 141 LeuGluArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMet 160  
 |||  
 Db 439 CTGAGCGCAGGCTGTACCGTGTTCCTTAGCTGTGTGTGTGTGTGTGTGTGTGTGTG 498  
 QY 161 Gly 161  
 |||  
 Db 499 GGC 501

## RESULT 4

AD28771  
 ID AAD28771 standard; cDNA; 644 BP.

XX AAD28771;

DT 07-MAY-2002 (first entry)

DE Human Interleukin-17 like (IL-17L) cDNA.

XX Human; interleukin-17 like; IL-17L; immune system dysfunction; diabetes;  
 KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;  
 KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;  
 KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;  
 KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
 KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
 KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
 KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
 KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
 KW cancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 159..644

FT /\*tag- a

FT /product- "Human IL-17L protein"

FT 159..206

FT /\*tag- b

FT 207..641

FT /\*tag- c

FT /product- "Mature IL-17L protein"

XX W0200208285-A2.

PN 31-JAN-2002.

XX 21-JUN-2001; 2001WO-US19861.

XX 22-JUN-2000; 2000US-213125P.

PR 02-FEB-2001; 2001US-266159P.

PR 16-MAR-2001; 2001US-0810384.

XX (AMGE-) AMGEN INC.

XX Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;

PI WPI; 2002-155217/20.

XX P-PSDB; AAE18120.

XX Nucleic acid molecules encoding Interleukin 17 (IL-17) - like

XX polypeptides useful in the treatment, prevention and diagnosis of

PT diseases e.g. cancer

XX Claim 1; Fig 1; 242pp; English.

XX The invention relates to nucleic acid molecules encoding Interleukin 17

CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
 CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,  
 CC preventing or ameliorating a disease, such as immune system dysfunction  
 CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);  
 CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel  
 CC disease, transplant rejection, graft vs host disease); infections (HIV,  
 CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,  
 CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
 CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin  
 CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
 CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy  
 CC atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma  
 CC leukaemia); reproductive (infertility, miscarriage, endometriosis), eye  
 CC (blindness, retinal neuropathy) and treatment of diseases involving  
 CC inflammation. The present sequence is human Interleukin-17 like (IL-17L)  
 CC cDNA.

XX Sequence 644 BP; 144 A; 204 C; 173 G; 123 T; 0 other;

## Alignment Scores:

Pred. No.: 4.1e-74 Length: 644  
 Score: 910.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0

US-10-037-591A-2 (1-161) x AAD28771 (1-644)

QY 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrp 20

Db 159 ATGTACACGAGTGGTGTGATCTTGGCAATGTCATGGAGACCCACACCTACAGCCACTGG 218

QY 21 ProSerCysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThr 40

Db 219 CCCAGCTGCTGCCCCAGCAAGGGCAGGACACCTCTGAGGAGCTCTGAGGTGGAGCACT 278

QY 41 ValProValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAla 60

Db 279 GTGCCTGTGCTCCCTAGAGCCTGCTAGGCCCAACCCAGAGTCTGTAGGGGCC 338

QY 61 SerGluAspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArg 80

Db 339 AGTGAAGATGGACCCCTCAACAGCAGGAGGCCATCTCCCTGGAGATATGAGTTGGACAGA 398

QY 81 AspLeuAsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysVal 100

Db 399 GACTTGAACCGGCTCCCGCAGGACCTGTACAGGCCGCTGTGCTGTGCCCGCAGTGC 458

QY 101 SerLeuGlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsn 120

Db 459 AGCCTACAGACAGGCTCCACATGGACCCCGGGGCACCTCGGAGCTGCTCTACCAACAAC 518

QY 121 GlnThrValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140

Db 519 CAGACTGTCTTCTACCGCGCGCGCATGCGTGGAGAGGGGACCCACAGGGGCTACTGC 578

QY 141 LeuGluArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMet 160

Db 579 CTGGAGCGCAGGCTGCTACCGTGTTCCTTAGCTGTGTGTGTGTGTGTGTGTGTGTGTG 638

QY 161 Gly 161

Db 639 GGC 641

XX RESULT 5

XX ABA03213

ID ABA03213 standard; cDNA; 644 BP.

XX AC ABA03213;  
 XX DT 11-FEB-2002 (first entry)  
 XX DE Human IL-17 receptor like protein ligand, IL-17E, coding sequence.  
 XX KW Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic;  
 KW antiporiatic; antimicrobial; anorectic; nootropic; neuroprotective;  
 KW antiasthmatic; anti-allergic; dermatological; cytostatic; gene therapy;  
 KW interleukin 17; immune system disorder; infection; weight; reproductive;  
 KW neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation;  
 KW glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;  
 KW tumour; IL-17E; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT CDS 159..644  
 FT /tag= a  
 FT /product= "Human IL-17E"  
 XX PN WO200168705-A2.  
 XX 20-SEP-2001.  
 XX 16-MAR-2001; 2001WO-US08688.  
 XX 16-MAR-2000; 2000US-189923P.  
 XX 12-MAY-2000; 2000US-204208P.  
 XX 27-NOV-2000; 2000US-0723232.  
 XX 02-FEB-2001; 2001US-266159P.  
 XX (AMGE-) AMGEN INC.  
 XX PI Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ;  
 XX WPI; 2002-055100/07.  
 XX DR P-PSDB; AAM47464.  
 XX Three human nucleic acids encoding interleukin 17 (IL-17) receptor like  
 PT polypeptides, useful for treating, diagnosing, ameliorating or  
 PT preventing immune system disorders (e.g. psoriatic arthritis) and  
 PT infections (e.g. viral infections).  
 XX Example 9; Page 233-234; 239pp; English.  
 XX The present invention relates to novel human nucleic acids encoding  
 CC interleukin 17 (IL-17) receptor like proteins (see ABA03200-ABA03202,  
 CC AAM47456, AAM47458 and AAM47459). The IL-17 receptor-like proteins and  
 CC coding sequences are useful for treating a pathological condition related  
 CC to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.  
 CC viral infections), weight disorders (e.g. obesity), neuronal dysfunction  
 CC disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin  
 CC disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),  
 CC bone disease (e.g. osteoporosis), vascular system disorders (e.g.  
 CC ischaemia), eye disorders, reproductive disorders, tumours and  
 CC inflammation. The present sequence is the coding sequence for IL-17E, a  
 CC human IL-17 receptor like protein ligand.  
 XX SQ Sequence 644 BP; 144 A; 204 C; 173 G; 123 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 4,1e-74 Length: 644  
 Score: 910.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
 US-10-037-591A-2 (1-161) x ABA03213 (1-644)  
 QY 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrp 20

Db 159 ATGTACAGGTGTTGCAATTTGGCAATGTCATGGAAACCCACACCTACAGCCACTGG 218  
 QY 21 ProSerCysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTyrSerThr 40  
 Db 219 CCCAGTGTGCTGCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 278  
 QY 41 ValProValProLeuLeuGluProAlaAaGProAsnArghisProGluSerCysArgAla 60  
 Db 279 GTGCTGTGCTGCCCTAGAGCTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 338  
 QY 61 SerGluAspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArg 80  
 Db 339 ACTGAAGATGGACCCCTCAACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 398  
 QY 81 AspLeuAsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysVal 100  
 Db 399 GACTTGACCGGCTCCCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 458  
 QY 101 SerLeuGlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsn 120  
 Db 459 AGCCTACAGCAGGAGGCTCCACATGGACCCCGGGGCAACTCGGAGGCTGCTCTACCAAC 518  
 QY 121 GlnThrValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140  
 Db 519 CAGACTGTCTTACCGGCGGCGCATGCCATGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 578  
 QY 141 LeuGluArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMet 160  
 Db 579 CTGAGCGCAGGAGTGTACCGTGTCTTCTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 638  
 QY 161 Gly 161  
 Db 639 GGC 641  
 RESULT 6  
 AAS09511  
 ID AAS09511 standard; cDNA; 1320 BP.  
 AC AAS09511;  
 DT 24-OCT-2001 (first entry)  
 DE Human cDNA encoding Interleukin 17E ligand, IL-17E.  
 KW Human; Interleukin-17E ligand; IL-17E; agonist; antagonist; ss;  
 KW PRO10272; DNA 147531-2821; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;  
 KW allergic disease; asthma; demyelinating disease;  
 KW degenerative cartilaginous disorder; transplantation associated disease.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 259..791  
 FT /tag= a  
 FT /product= "IL-17E"  
 FT sig\_peptide 259..357  
 FT /tag= b  
 FT mat\_peptide 358..788  
 FT /tag= c  
 FT /label= Mature\_IL\_17E  
 XX WO200146420-A2.  
 XX 28-JUN-2001.  
 XX 20-DEC-2000; 2000WO-US34956.  
 XX 23-DEC-1999; 99US-0172096.  
 XX 30-DEC-1999; 99WO-US31274.  
 XX 11-JAN-2000; 2000US-0175481.  
 XX 18-FEB-2000; 2000WO-US04341.

PR 02-MAR-2000; 2000WO-US05841.  
 PR 21-MAR-2000; 2000US-0191007.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 22-JUN-2000; 2000US-0213087.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 24-OCT-2000; 2000US-0242837.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 28-NOV-2000; 2000US-0253646.  
 PR 01-DEC-2000; 2000WO-US32678.

(GETH ) GENENTECH INC.

PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;  
 PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL;  
 PI Watanabe CK, Williams PM, Wood WI, Yansura DG;

DR WPI; 2001-451708/48.  
 DR P-PSDB; AAU04952.

XX Novel PRO polypeptides homologous to interleukin-17, useful for the  
 PT diagnosis and treatment of immune related disease e.g. rheumatoid  
 PT arthritis and diabetes

XX Claim 1; Fig 5; 188pp; English.

XX The sequence (DNA 147531-2821) encodes a PRO polypeptide (PRO10272)  
 CC which is the human Interleukin 17E ligand, IL-17E. A composition  
 CC containing ant/agonists to the PRO polypeptides or individual components  
 CC are useful for treating a mammal with an immune related disease, e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, a demyelinating disease, an autoimmune or immune-mediated skin  
 CC disease, contact dermatitis, an allergic disease e.g. food  
 CC hypersensitivity, asthma, a transplantation associated disease, or a  
 CC chronic inflammatory demyelinating polyneuropathy. Treating a  
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or  
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous  
 CC examples of the diseases and disorders are given in the specification.

XX Sequence 1320 BP; 280 A; 353 C; 384 G; 303 T; 0 other;

#### Alignment Scores:

Pred. No.: 1.27e-72 Length: 1320  
 Score: 898.00 Matches: 159  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.68% Indels: 0  
 DB: 22 Gaps: 0

US-10-037-591A-2 (1-161) x AAS09511 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22  
 DB 313 CAGGTGGTGGATCTTGGCAATGGTCATGGACCCACACCTACAGCCACTGGCCGAC 372  
 QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42  
 DB 373 TGTGCCCCCAGCAAGGCGAGACACCTCTCAGGAGCTGCTGAGGTGGAGCACTGCGCT 432  
 QY 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62  
 DB 433 GTGGCTCCCTAGAGCTGTGAGGCCCAACCCGCCACAGAGTCTGTAGGGCCAGTGAA 492  
 QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82  
 DB 493 GATGACCCCTCAACAGCAGGCGCCATCTCCCTCGGAGATATGATTGGACAGACACTTG 552  
 QY 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102

Db 553 AACGGGTCCCCCAGGACCTGTACACGCCCTTGCTGTGCTGCCCGCACTGGCTACGCTA 612  
 QY 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122  
 Db 613 CAGACAGCTCCACATGAGCCCGGGCAACTCGGAGCTGCTTACCACAAACCACT 672  
 QY 123 ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142  
 Db 673 GTCTTCTACAGGCGGCCATGCCATGGGAGAGGACCCACAGGGCTACTGCGCTGGAG 732  
 QY 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161  
 Db 733 CGCAGGCTGTACCGTGTCTTACCTTGTGTGTGTGGGCCCGCTGTGTATGATGATG 789

#### RESULT 7

AAC85969

ID AAC85969 standard; cDNA; 1320 BP.

XX AAC85969;

XX 22-AUG-2001 (first entry)

DE Native sequence of PRO10272 cDNA, clone DNA147531-2821..

XX PRO; PRO1081; PRO1274; PRO10272; proliferation; T-lymphocyte;  
 KW PRO199; PRO1556; PRO4401; PRO10268; inhibition; stimulation;  
 KW infiltration; mononuclear cell; eosinophil; erythema multiforme;  
 KW polymorphonuclear neutrophil; PMN; antibody; immune-related disorder;  
 KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;  
 KW juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; skin disease;  
 KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia; asthma;  
 KW autoimmune thrombocytopaenia; thyroiditis; diabetes mellitus; allergy;  
 KW immune-mediated renal disease; demyelination; central nervous system;  
 KW peripheral nervous system; idiopathic demyelinating polyneuropathy;  
 KW Guillain-Barre syndrome; hepatobiliary disease; eosinophilic pneumonia;  
 KW chronic active hepatitis; primary biliary cirrhosis; allergic rhinitis;  
 KW granulomatous hepatitis; sclerosing cholangitis; food hypersensitivity;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy; urticaria;  
 KW Whipple's disease; idiopathic pulmonary fibrosis; contact dermatitis;  
 KW psoriasis; atopic dermatitis; hypersensitivity pneumonitis;  
 KW graft rejection; graft-versus-host disease; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	259..792
	/*tag= a
sig_peptide	/product= "PRO10272 polypeptide"
	259..354
	/*tag= b
mat_peptide	355..769
	/*tag= c

WO200140465-A2.

07-JUN-2001.

10-NOV-2000; 2000WO-US30873.

30-NOV-1999; 99WO-US28313.

09-DEC-1999; 99US-0170262.

23-DEC-1999; 99US-0172059.

11-JAN-2000; 2000US-0175481.

20-JAN-2000; 2000US-0177118.

18-FEB-2000; 2000WO-US04342.

03-MAR-2000; 2000US-0187202.

30-MAY-2000; 2000WO-US14941.

05-JUN-2000; 2000US-0209832.

24-AUG-2000; 2000WO-US23328.

(GETH ) GENENTECH INC.







```

RESULT 10
AAA58988
ID   AAA58988 standard; cDNA; 985 BP.
XX
AC   AAA58988;
XX
DT   07-NOV-2000 (first entry)
DE
DE   cDNA encoding a murine interleukin (IL) 174 polypeptide.
XX
KW   Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
KW   IL-177; IL-171; cell proliferation; cancer; ss.
XX
OS   Mus sp.
XX
FH   Key
FH   CDS
FT   sig_peptide
FT   mat_peptide
XX
XX   WO200042188-A2.
XX
XX   20-JUL-2000.
XX
XX   10-JAN-2000; 2000WO-US00006.
XX
XX   11-JAN-1999; 99US-0228822.
XX
XX   (SCHE ) SCHERING CORP.
XX
XX   Gorman DM, Bazan JF, Kastelein RA;
XX
XX   WPI; 2000-466130/40.
XX
XX   P-PSDB; AAB07600.
XX
XX   New isolated polynucleotide encoding a mammalian Interleukin-17 like
XX   protein used to identify genes for homologous proteins -
XX
XX   Disclosure; Page 18; 11lpp; English.
XX
XX   The present sequence encodes an interleukin-174 (IL-174) polypeptide.
XX   The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a
XX   member of a new group of interleukins, IL-170 polypeptides. The members
XX   comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
XX   protein can be used to treat abnormal proliferation e.g. cancer
XX   or degenerative conditions. Antibodies can be used in diagnostic
XX   methods to detect over production of IL-170 protein in cells or body
XX   fluids.
XX
XX   SQ   Sequence 985 BP; 199 A; 296 C; 268 G; 222 T; 0 other;

Alignment Scores:
Pred. No.:      1,55e-55      Length:      985
Score:          709.00      Matches:      129
Percent Similarity: 82.14%      Conservative: 9
Best Local Similarity: 76.79%      Mismatches: 22
Query Match:    77.91%      Indels:      8
DB:             21          Gaps:       1

US-10-037-591A-2 (1-161) x AAA58988 (1-985)
Oy   1   MetTyrGlnValAlaPheLeuAlaMetValMetGlyThrHisThrTyr----- 17
Db   1   ATGTACCAAGGCTGTTCATCTTGGCATGATCGTGGGAACCCACACCTCAGCTGCGG 60
Oy   18  -----SerHisTyrProSerCysProSerLysGlyGlnAspThrSer 32
Db   61  ATCCAGGAGGCTGTCAGTCACTTGTCCAGCTGCTCCCGCAGCAAGAGCAAGACCCCGG 120

33  GluGluLeuLeuArgTyrSerThrValProValProLeuGluProAlaArgProAsn 52
121 GAGAGTGGCTGAAGTGGAGCTCTGCATCTGTGTCTCCCGCCAGAGCCTCTGAGCCACACC 180
53  ArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIleSer 72
181 CACCACGACAGATCCTGCAGGGCCAGCAAGGATGCGCCCTCAACAGCAGGCGCATCTCT 240
73  ProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHisAla 92
241 CCTTGGAGCTATGAGTTGGACAGGACTTGAATCGGTCTCCCGCAGGACCTGTACCACGCT 300
93  ArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGly 112
301 CGATGCTGTGCCACACACTGCTGACGCTACAGACAGGCTCCACATGGACCCGCTGGGC 360
113 AsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCysHisGlyGlu 132
361 AACTCGCTCCCACTTTACCACACACAGACAGCGTCTTCTACCGGGCGCATGCGTGTGAG 420
133 LysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArgValSerLeuAlaCys 152
421 GAAGGTACCCATCGCGCTACTGCTTGGAGCGCAGGCTCTACCGAGTCTCCTTGGCTTGT 480
153 ValCysValArgProArgValMet 160
481 GTGTGTGTGGCGCCCGGGTCAATG 504

RESULT 11
AAA59160
ID   AAA59160 standard; cDNA; 985 BP.
XX
AC   AAA59160;
XX
DT   07-NOV-2000 (first entry)
DE
DE   cDNA encoding a murine interleukin-174 polypeptide.
XX
KW   Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;
KW   IL-174; IL-176; IL-177; cell proliferation; cancer; ss.
XX
OS   Mus sp.
XX
FH   Key
FH   CDS
FT   sig_peptide
FT   mat_peptide
XX
XX   WO200042187-A1.
XX
XX   20-JUL-2000.
XX
XX   10-JAN-2000; 2000WO-US00005.
XX
XX   11-JAN-1999; 99US-0229402.
XX
XX   (SCHE ) SCHERING CORP.
XX
XX   Gorman DM, Bazan JF, Kastelein RA;
XX
XX   WPI; 2000-476060/41.
XX
XX   P-PSDB; AAB07694.
XX
XX   New DNA sequence encoding a mammalian homolog of CTLA-8, designated
XX   interleukin-171 (IL-171), useful for recombinant production of IL-171
XX   which can be used for treating conditions associated with abnormal
XX   physiology or development -
XX
XX   Disclosure; Page 21; 11lpp; English.
PS
```

XX The present sequence encodes an interleukin (IL)-174 polypeptide.  
 CC It is a mammalian homologue of the cytokine designated CTLA-8 (also  
 CC referred to as IL-17). The specification also describes homologues  
 CC IL-171, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
 CC sequence encoding IL-171 is useful for identifying genes, mRNA and  
 CC cDNA molecules which code for related or homologous proteins. The  
 CC IL-171 protein, antibodies against IL-171, and compounds which have  
 CC binding affinity to IL-171 are useful in treatment of conditions  
 CC associated with abnormal physiology or development, including abnormal  
 CC proliferation, e.g. cancerous conditions, or degenerative conditions.  
 CC The IL-171 protein can be used in kits and assay methods for identifying  
 CC compounds that selectively bind to IL-171.

XX SQ Sequence 985 BP; 199 A; 296 C; 268 G; 222 T; 0 other;

Alignment Scores:  
 Pred. No.: 1.55e-55 Length: 985  
 Score: 709.00 Matches: 129  
 Percent Similarity: 82.14% Conservative: 9  
 Best Local Similarity: 76.79% Mismatches: 22  
 Query Match: 77.91% Indels: 8  
 DB: 21 Gaps: 1

US-10-037-591A-2 (1-161) x AAA59160 (1-985)

Qy 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyr----- 17  
 Db 1 ATGTACAGGCTGTGTCATCTTGGCATGATCGTGGGAACCCACACCGTCAGCTGCGG 60  
 Qy 18 -----SerHisTrpProSerCysProSerLysGlyClnAspThrSer 32  
 Db 61 ATCCAGGAGGGTGCAGTCACCTGTCGCCAGCTGCTGCCAGCAAGAGCAAGACCCCG 120  
 Qy 33 GluGluLeuLeuArgTrpSerThrValProValProLeuGluProAlaArgProAsn 52  
 Db 121 GAGGAGTGGCTGAATGGAGCTGCTGCATCTGTGTCTCCCGCCAGAGCCCTCTGAGCCACACC 180  
 Qy 53 ArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIleSer 72  
 Db 181 CACACGCGAGATCTCTGAGGCCAGCAAGATGCGCCCTCAACAGCAGGCGCATCTCT 240  
 Qy 73 ProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHisAla 92  
 Db 241 CTTTGGAGCTATGATGGAGAGGACTTGAATCGGGTCCCGCCAGGACCTGTACCCAGCT 300  
 Qy 93 ArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGly 112  
 Db 301 CGATCCCTGTGCCACACTGCTGACCTACAGAGGCTCCCATGAGCCCGCTGGGCG 360  
 Qy 113 AsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCysHisGlyGlu 132  
 Db 361 AACTCCGTCCTCCACTTACCAACACAGAGCGTCTTCTACCGCGCGCCATGCCATGGTGAG 420  
 Qy 133 LysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArgValSerLeuAlaCys 152  
 Db 421 GAAGGTACCATCCGCGCTACTGCTTGGAGCGCAGGCTCTACCGAGTCTCCCTGGCTGT 480  
 Qy 153 ValCysValArgProArgValMet 160  
 Db 481 CTGTGTGTGCGGCGCGGTCATG 504  
 RESULT 12  
 ABA02394  
 ID ABA02394 standard; DNA; 985 BP.  
 AC ABA02394;  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE Murine interleukin 174 (IL-174)-encoding DNA.  
 XX  
 KW Mouse; murine; interleukin 174; IL-174; cytokine; Th2 response;

KW innate immune response; inflammation; gut cell growth;  
 KW extramedullary hematopoiesis; antibody response; granuloma formation;  
 KW autoimmune condition; multiple sclerosis; systemic lupus erythematosus;  
 KW rheumatoid arthritis; diabetes; psoriasis; infectious agent;  
 KW inflammatory condition; Crohn's disease; ulcerative colitis;  
 KW pancreatitis; hepatitis; allergy; Th2-mediated condition;  
 KW systemic anaphylactic response; skin hypersensitivity response;  
 KW dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator;  
 KW antiinflammatory; antiarthritic; antidiabetic; antifungal;  
 KW dermatological; neuroprotective; anti-allergic; agonist; antagonist; ds.  
 XX Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..510  
 FT /\*tag= a  
 FT /product= "Murine IL-174"  
 FT sig\_peptide 1..48  
 FT /\*tag= b  
 FT mat\_peptide 49..507  
 FT /\*tag= c  
 FT /product= "Mature murine IL-174"  
 XX  
 PN WO200179288-A2.  
 XX  
 XX 25-OCT-2001.  
 XX  
 PF 17-APR-2001; 2001WO-US12493.  
 XX  
 PR 18-APR-2000; 2000US-198488P.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 PI Hurst SD, Zurawski SM, Rennick DM;  
 XX  
 DR WPI: 2002-034343/04.  
 DR P-P5DB; AAM52692.  
 XX  
 PT Administering an interleukin 174 agonist or antagonist to a mammal  
 PT regulates various immune and inflammatory responses and is useful to  
 PT treat for example autoimmune diseases, allergies or response to an  
 PT infection  
 XX  
 PS Disclosure: Page 28-29; 29pp; English.  
 CC  
 CC The invention relates to methods of directing an immune response in a  
 CC mammal by the administration of an agonist or antagonist of the cytokine  
 CC interleukin 174 (IL-174). Administration of an IL-174 agonist directs the  
 CC immune response towards a Th2 response, stimulates an innate immune  
 CC response, augments the inflammatory response from epithelial or  
 CC fibroblast cells, induces gut cell growth, promotes extramedullary  
 CC haematopoiesis, or augments an antibody response in serum and faecal  
 CC material, while administration of an IL-174 antagonist directs the immune  
 CC response away from a Th2 type response, and prevents inflammation or  
 CC granuloma formation. IL-174 agonists may be used to treat autoimmune  
 CC conditions (particularly multiple sclerosis, systemic lupus  
 CC erythematosus, rheumatoid arthritis, diabetes or psoriasis), a response  
 CC to an infectious agent, or inflammatory conditions such as Crohn's  
 CC disease, ulcerative colitis, pancreatitis, or hepatitis. IL-174  
 CC antagonists may be used to treat inflammatory, allergic or Th2-mediated  
 CC conditions (e.g., systemic anaphylactic response, skin hypersensitivity  
 CC response, dermatitis, asthma, fibrosis, or eosinophilic gastritis). The  
 CC present sequence represents DNA encoding murine IL-174.

XX SQ Sequence 985 BP; 199 A; 296 C; 268 G; 222 T; 0 other;

Alignment Scores:

Pred. No.: 1.55e-55 Length: 985  
 Score: 709.00 Matches: 129  
 Percent Similarity: 82.14% Conservative: 9  
 Best Local Similarity: 76.79% Mismatches: 22  
 Query Match: 77.91% Indels: 8  
 DB: 21 Gaps: 1





```
XX WO200042188-A2.
XX
XX PD
XX
XX 20-JUL-2000.
XX
XX 10-JAN-2000; 2000WO-US000006.
XX
XX 11-JAN-1999; 99US-0228822.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Gorman DM, Bazan JF, Kastelein RA;
XX
XX WPI; 2000-466130/40.
XX
XX P-PSDB; AAB07599.
XX
XX New isolated polynucleotide encoding a mammalian Interleukin-17 like
XX protein used to identify genes for homologous proteins -
XX
XX PS
XX
XX Disclosure; Page 17; 111pp; English.
XX
XX The present sequence encodes an interleukin-174 (IL-174) polypeptide.
XX The polypeptide is an IL-17-like (CtUA-8 related) protein. It is a
XX member of a new group of interleukins, IL-170 polypeptides. The members
XX comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
XX protein can be used to treat abnormal proliferation e.g. cancer
XX or degenerative conditions. Antibodies can be used in diagnostic
XX methods to detect over production of IL-170 protein in cells or body
XX fluids.
XX
XX SQ Sequence 620 BP; 125 A; 183 C; 188 G; 124 T; 0 other;

Alignment Scores:
Pred. No.: 4,45e-36 Length: 620
Score: 493.00 Matches: 100
Percent Similarity: 84.25% Conservative: 7
Best Local Similarity: 78.74% Mismatches: 20
Query Match: 54.18% Indels: 3
DB: 21 Gaps: 0

US-10-037-591A-2 (1-161) x AAA58987 (1-620)
QY 34 GluLeuLeuArgTrpSerThrValProValProLeuGluProAlaArgProAsnArg 53
   ||| |||:|||||:|:| ||| |||
Db 26 GAGTGGCTGAAGTGGAGCTCTGATCTATCCGCCCCAGAGCCCTCTGAGCCACACCCAC 85
QY 54 HisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIleSerPro 73
   ||| |||:|||||:|:| ||| |||
Db 86 CACGCAGAAATCTGCAGGCGCCAGCAAGGATGG-CCTCTCAACAGCAGGCGCCATCTCTCT 144
QY 74 TrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHisAlaArg 93
   ||| |||:|||||:|:| ||| |||
Db 145 TGGAGCTATGATGGACAGGACTTGAATCGGGTCCCGCCAGGACTGGTACCCACGCTCGA 204
QY 94 CysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGlyAsn 113
   ||| |||:|||||:|:| ||| |||
Db 205 TGCCTGTGCCACACTGGCTCAGCTACAGAGCTCCACATGGACCCCGCTGGGCAAC 264
QY 114 SerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCysHisGlyGlyLys 133
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Db 265 TCCGTCCCACTTTACCAACAACAGACGGCTTCTTACCGGCGGCCATGCAT-GGCGAGGAA 323
QY 134 GlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArgValSerLeuAlaCysVal 153
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Db 324 GGTACCCCATCCCGCTACTGCTTGGAGCGCAGGTC-TACCGAGTCTCTCTGGCTTGTGTG 382
QY 154 CysValArgProArgValMet 160
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Db 383 TGTGTGGCGGCCCGGGGTATG 403
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Search completed: May 12, 2003, 02:05:54  
Job time : 166 secs

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 00:33:18 ; Search time 163 Seconds  
(without alignments)  
8897.466 Million cell updates/sec

Title: US-10-037-591A-1

Perfect score: 644

Sequence: 1 ctcaagtcaactccctataaaaa.....ggccccgtgtgtaggctag 644

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_101002.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	100.0	644	24	AAD28771 Human Interleukin-
2	644	100.0	644	24	ABA03213 Human IL-17 recept
3	493	76.6	504	21	AAA58986 cDNA encoding a hu
4	493	76.6	504	21	AAA59158 Human Interleukin
5	493	76.6	504	24	ABA02393 Human cDNA encodin
6	478.4	74.3	1320	22	AAS09511 Native sequence of
7	478.4	74.3	1320	22	AAC85969 Human PRO10272 cDN
8	478.4	74.3	1320	22	AAF92135 DNA encoding novel
9	418.2	64.9	1355	23	AAS93559

10	336.8	52.3	1013	24	AAD28772	Mouse Interleukin-
11	336.2	52.2	1496	24	AAD28773	Mouse non-secreted
12	335.2	52.0	985	21	AAA58986	cDNA encoding a mu
13	335.2	52.0	985	21	AAA59160	Murine interleukin
14	335.2	52.0	985	24	ABA02394	cDNA encoding a mu
15	249.6	38.8	620	21	AAA58987	cDNA encoding a mu
16	249.6	38.8	620	21	AAA59159	cDNA encoding a mu
17	55.4	8.6	1067	21	AAZ36836	Nucleotide sequenc
18	55.4	8.6	1067	23	AAZ36836	Human interleukin
19	53.8	8.4	591	21	AAA09153	Human interleukin-
20	53.8	8.4	591	24	AAD38083	Human LP-48 gene.
21	53.8	8.4	1047	21	AAZ96338	cDNA encoding a no
22	53.8	8.4	1047	21	AAZ29728	Human Interleukin
23	53.8	8.4	1047	22	AAZ46148	Human DNA encoding
24	53.8	8.4	1047	22	AAZ46148	Human cDNA encodin
25	53.8	8.4	1107	21	AAA58991	cDNA encoding a hu
26	53.8	8.4	1107	21	AAA59149	cDNA encoding a hu
27	53.8	8.4	1177	22	AAD15291	Human Interleukin
28	45	7.0	45	22	AAS09523	Human IL-17E hybri
29	42	6.5	10732	21	AAA10594	Gene encoding a su
30	41.4	6.4	540	20	AAZ89401	Human interleukin-
31	41.4	6.4	543	21	AAA58980	cDNA encoding a hu
32	41.4	6.4	543	21	AAA59152	cDNA encoding a hu
33	41.4	6.4	687	20	AAZ34282	Human PRO1031 nucl
34	41.4	6.4	687	21	AAZ78577	Human PRO1031 (UNO
35	41.4	6.4	687	21	AAZ75694	cDNA clone DNA5929
36	41.4	6.4	687	21	AAZ58608	Human PRO1031 prot
37	41.4	6.4	687	21	AAZ29727	Human Interleukin
38	41.4	6.4	687	22	AAS09509	Human cDNA encodin
39	41.4	6.4	687	22	AAZ21466	Human cDNA sequenc
40	41.4	6.4	687	22	AAZ91479	Human PRO1031 cDNA
41	41.4	6.4	687	22	AAZ88961	Human PRO1031 codi
42	41.4	6.4	689	21	AAZ95780	Human immune syste
43	41.4	6.4	704	22	AAZ79235	Human cell factor-
44	41.4	6.4	705	20	AAZ15870	cDNA encoding inte
45	41.4	6.4	705	21	AAZ75787	DNA encoding a hum

#### ALIGNMENTS

RESULT 1

AAD28771

ID AAD28771 standard; cDNA; 644 BP.

XX AAD28771;

AC AAD28771;

XX 07-MAY-2002 (first entry)

XX Human Interleukin-17 like (IL-17L) cDNA.

Human; interleukin-17 like; IL-17L; immune system dysfunction; diabetes; cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus; inflammatory bowel disease; neuronal dysfunction; transplant rejection; autoimmune disorder; lung; skin; kidney; bone; eye; vascular system; infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis; cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema; eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease; epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis; leukaemia; retinal neuropathy; infertility; miscarriage; inflammation; cancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
CDS 159..644

FT /tag- a

FT /product= "Human IL-17L protein"

FT sig\_peptide 159..206

FT /tag- b

FT mat\_peptide 207..641

FT /tag- c

FT /product= "Mature IL-17L protein"







RESULT 4	
AAA59158	
ID	AAA59158 standard; cDNA; 504 BP.
XX	
AC	AAA59158;
XX	
DT	07-NOV-2000 (first entry)
XX	
DE	cDNA encoding a human interleukin-174 polypeptide.
XX	
KW	Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;
XX	IL-174; IL-176; IL-177; cell proliferation; cancer; ss.

WO200042187-A1.  
XX  
XX  
PD 20-JUL-2000.  
XX  
XX 10-JAN-2000; 2000WO-US000005.  
XX  
XX 11-JAN-1999; 99US-0229402.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Gorman DM, Bazan JF, Kastelein RA;  
Fi  
XX  
XX WPI; 2000-476060/41.  
XX P-PSDB: AAB07692.  
DR

XX  
SQ Sequence 504 BP; 98 A; 165 C; 148 G; 93 T; 0 other;  
Query Match 76.6%; Score 493; DB 21; Length 504;

Query Match 76.6%; Score 493; DB 21; Length 504;

Best Local Similarity 99.8%; Pred. No. 1.4e-123;	
Matches 504; Conservative 0; Mismatches 0; Indels	
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Db	1 TGAGTGTGAGTG-CCAGCATGTACACAGGTGGTTCATTTCTTGGAATGGT
QY	200 CCACACTACAGCCACTGCGCCAGCTGCTGCCAGCAAGGCGAGGACAC
Db	60 CCACACTACAGCCACTGCGCCAGCTGCTGCCAGCAAGGCGAGGACACTCTGAGGA 119
QY	260 GCTGCTGAGGTGGAGCAGCTGTGCTGTGCTCTCCCTAGAGCCTGTAGGCCCAACCGCA 319
Db	120 GCTGCTGAGGTGGAGCAGCTGTGCTGTGCTCTCCCTAGAGCCTGTAGGCCCAACCGCA 179
QY	320 CCAGAGTCTGTAGGGCCAGTGAAGATGGACCCCTCAACACAGAGGGCCATCTCCCCCTG 379
Db	180 CCCAGAGTCTGTAGGGCCAGTGAAGATGGACCCCTCAACACAGAGGGCCATCTCCCCCTG 239
QY	380 GAGATATGAGTTGGACAGAGACTTTGAACCGGTCCCCAGGACCTGTACCCAGCCCGCTTG 439
Db	240 GAGATATGAGTTGGACAGAGACTTTGAACCGGTCCCCAGGACCTGTACCCAGCCCGCTTG 299
QY	440 CCTGTGCCCCACTGGGTAGCCTACAGACAGGCTCCACATGGACCCCGGGGCACTC 499
Db	300 CCTGTGCCCCACTGGGTAGCCTACAGACAGGCTCCACATGGACCCCGGGGCACTC 359
QY	500 GGAGCTGCTCTACACAAACAGACTGTCTTCTACGGGGGCCATGCCATGGCGAGAAGG 559
Db	360 GGAGCTGCTCTACACAAACAGACTGTCTTCTACGGGGGCCATGCCATGGCGAGAAGG 419
QY	560 CACCACAAGGGTACTGCTGGAGCGCAGGCTGTACCGCTGTTTCTTACGTTGTGTGTG 619
Db	420 CACCACAAGGGTACTGCTGGAGCGCAGGCTGTACCGCTGTTTCTTACGTTGTGTGTG 479
QY	620 TGTGCGGCCCCGTGTGATGGGCTAG 644
Db	480 TGTGCGGCCCCGTGTGATGGGCTAG 504

AA  
AC ABA02393;

26-FEB-2002 (first entry)

Human interleukin 174 (IL-174)-encoding DNA.

Human; interleukin 174; IL-174; cytokine; Th2 response;  
innate immune response; inflammation; gut cell growth;  
extramedullary haematopoiesis; antibody response; granuloma formation;  
autoimmune condition; multiple sclerosis; systemic lupus erythematosus;  
rheumatoid arthritis; diabetes; psoriasis; infectious agent;  
inflammatory condition; Crohn's disease; ulcerative colitis;  
pancreatitis; hepatitis; allergy; Th2-mediated condition;  
systemic anaphylactic response; skin hypersensitivity response;  
dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator;  
antiinflammatory; antiarthritic; antidiabetic; antifungal;  
dermatological; neuroprotective; antiallergic; agonist; antagonist; ds.  
Homo sapiens.

OS . Homo sapiens.

XX	Key	Location/Qualifiers
FH		

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CDS
19:304
/*tag= a

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FT	product="Human IL-1/4"
1	10 55
2	10 55

FT / \*tag= b

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FT      /*tag= c

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FT /product= "Mature human IL-174"















[illegible]



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2003, 01:11:39 ; Search time 44 Seconds  
(without alignments)  
487.576 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MYQVAFSLAMVMTGTHYSHW.....ERRLYRSLACVCRPRVMG 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	910	100.0	161	21	A human interleukin
2	910	100.0	161	21	A human interleukin
3	910	100.0	161	23	Human interleukin
4	910	100.0	161	23	Human interleukin
5	910	100.0	161	23	Human IL-17 recept
6	898	98.7	177	22	Human interleukin
7	898	98.7	177	22	PRO10272 polypepti
8	898	98.7	177	22	Human PRO10272. H
9	834	91.6	350	22	Novel human diagno
10	709	77.9	169	21	A murine interleuk

11	709	77.9	169	21	AA07694	A murine interleuk
12	709	77.9	169	23	AAE18121	Mouse Interleukin-
13	709	77.9	169	23	AA052692	Murine Interleukin
14	670	73.6	160	23	AAE18122	Mouse non-secreted
15	351.5	38.6	144	21	AA07599	A murine interleuk
16	351.5	38.6	144	21	AA07693	A murine interleuk
17	170.5	18.7	206	21	AA07693	Human Interleukin
18	165.5	18.2	187	23	AA04485	Human Interleukin
19	165.5	18.2	197	21	AA023794	Mature human LP-48
20	165.5	18.2	197	21	AA018911	A novel polypeptid
21	165.5	18.2	197	21	AA07602	A human interleuki
22	165.5	18.2	197	21	AA07684	A human interleuki
23	165.5	18.2	197	21	AA092338	Human Interleukin-
24	165.5	18.2	197	21	AA04460	Human Interleukin
25	165.5	18.2	197	21	AA053892	Amino acid sequenc
26	165.5	18.2	197	22	AA066121	Human Interleukin
27	165.5	18.2	197	22	AA029247	Human PRO polypept
28	165.5	18.2	197	22	AA04951	Human Interleukin
29	165.5	18.2	197	23	AA023792	Human LP-48 protel
30	165.5	18.2	227	22	AA08676	Human Interleukin
31	165.5	18.2	227	22	AA08679	Human Interleukin
32	165.5	18.2	227	22	AA08680	Human Interleukin
33	165.5	18.2	227	22	AA08681	Human Interleukin
34	165.5	18.2	227	22	AA08682	Human Interleukin
35	165.5	18.2	227	22	AA08683	Human Interleukin
36	165.5	18.2	227	22	AA08684	Human Interleukin
37	165	18.1	425	21	AA04462	Human Interleukin
38	163.5	18.0	223	22	AA08677	Human mature inter
39	161.5	17.7	227	22	AA08685	Human Interleukin
40	160.5	17.6	227	22	AA08687	Human Interleukin
41	157.5	17.3	227	22	AA08686	Human Interleukin
42	156.5	17.2	227	22	AA08690	Human Interleukin
43	156.5	17.2	227	22	AA08688	Human Interleukin
44	156.5	17.2	227	22	AA08689	Human Interleukin
45	156.5	17.2	227	22	AA08691	Human Interleukin
			227	22	AA08693	Human Interleukin

#### ALIGNMENTS

RESULT 1

AA07598

ID AA07598 standard; Protein; 161 AA.

XX AA07598;

AC AA07598;

XX DT 07-NOV-2000 (first entry)

XX A human Interleukin (IL) 174 polypeptide.

XX Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;

KW IL-177; IL-171; cell proliferation; cancer.

XX Homo sapiens.

OS Homo sapiens.

PH Key

FT Peptide

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Protein

FT Modified-site

FT Modified-site

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FT Modified-site

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XX (SCHE ) SCHERING CORP.  
XX  
XX Gorman DM, Bazan JF, Kastelein RA;  
XX  
XX WPI; 2000-466130/40.  
XX  
XX N-PSDB; AAA58986.  
XX  
XX New isolated polynucleotide encoding a mammalian Interleukin-17 like  
XX protein used to identify genes for homologous proteins  
XX  
XX Claim 11; Page 16; 11lpp; English.  
XX  
XX The present sequence represents an interleukin-174 (IL-174) polypeptide.  
XX CC The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a  
XX CC member of a new group of interleukins, IL-170 polypeptides. The members  
XX CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170  
XX CC protein can be used to treat abnormal proliferation e.g. cancer  
XX CC or degenerative conditions. Antibodies can be used in diagnostic  
XX CC methods to detect over production of IL-170 protein in cells or body  
XX CC fluids.  
XX  
XX Sequence 161 AA;  
SQ  
Query Match 100.0%; Score 910; DB 21; Length 161;  
Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MYQVAFAMVGMGTHYSHWPSCCPSKQDTSELLRWSTVPVPPLEPARNRHPSERA 60  
QY 61 SEDGPLNSRAISPRYELDRDLNRLPDQLYHARCLPHCVSLQTGSHWDPGRNSELHYHN 120  
Db 61 SEDGPLNSRAISPRYELDRDLNRLPDQLYHARCLPHCVSLQTGSHWDPGRNSELHYHN 120

QY 121 QTVEYRRPCHGEKTHKGYCLERLYRVSLACVCRPRVMG 161  
Db 121 QTVEYRRPCHGEKTHKGYCLERLYRVSLACVCRPRVMG 161  
RESULT 2  
AAB07692  
ID AAB07692 standard; Protein; 161 AA.  
XX  
XX AAB07692;  
XX  
XX 07-NOV-2000 (first entry)  
XX  
XX A human interleukin-174 polypeptide.  
XX  
XX Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;  
XX IL-174; IL-176; IL-177; cell proliferation; cancer.  
XX  
XX Homo sapiens.  
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XX 11-JAN-1999; 99US-0229402.  
 PR (SCHE ) SCHERING CORP.  
 PA Gorman DM, Bazan JF, Kastelein RA;  
 XX WPI; 2000-476060/41.  
 XX N-PSDB; AAA59158.  
 XX New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
 PT interleukin-171 (IL-171), useful for recombinant production of IL-171  
 PT which can be used for treating conditions associated with abnormal  
 PT physiology or development -  
 XX Disclosure; Page 19; 11pp; English.  
 PS The present sequence represents an interleukin (IL)-174 polypeptide.  
 CC It is a mammalian homologue of the cytokine designated CTLA-8 (also  
 CC referred to as IL-17). The specification also describes homologues  
 CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
 CC sequence encoding IL-171 is useful for identifying genes, mRNA and  
 CC cDNA molecules which code for related or homologous proteins. The  
 CC IL-171 protein, antibodies against IL-171, and compounds which have  
 CC binding affinity to IL-171 are useful in treatment of conditions  
 CC associated with abnormal physiology or development, including abnormal  
 CC proliferation, e.g. cancerous conditions, or degenerative conditions.  
 CC The IL-171 protein can be used in kits and assay methods for identifying  
 CC compounds that selectively bind to IL-171.  
 XX Sequence 161 AA;  
 SQ  
 Query Match 100.0%; Score 910; DB 21; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MYQVAFAMVWGTHYTHSWPSCCPKSGQDTSEELLRWSTVPVPPLEPARNRHPESCRA 60  
 DB 1 MYQVAFAMVWGTHYTHSWPSCCPKSGQDTSEELLRWSTVPVPPLEPARNRHPESCRA 60  
 QY 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLCPHCVSLOTGSHMDPRGNSSELYHN 120  
 DB 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLCPHCVSLOTGSHMDPRGNSSELYHN 120  
 QY 121 QTVFYRRCPCHGKGTGKCYCLERRLYRVSLACVCRVRVMG 161  
 DB 121 QTVFYRRCPCHGKGTGKCYCLERRLYRVSLACVCRVRVMG 161  
 QY 121 QTVFYRRCPCHGKGTGKCYCLERRLYRVSLACVCRVRVMG 161  
 DB 121 QTVFYRRCPCHGKGTGKCYCLERRLYRVSLACVCRVRVMG 161  
 RESULT 3  
 ID AAE18120 standard; Protein; 161 AA.  
 XX AAE18120;  
 XX 07-MAY-2002 (first entry)  
 XX Human Interleukin-17 like (IL-17L) protein.  
 DE Human; interleukin-17 like; IL-17L; immune system dysfunction; diabetes;  
 KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;  
 KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;  
 KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;  
 KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
 KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
 KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
 KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
 KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
 KW cancer.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH

FT Peptide 1..16 /label= Signal\_peptide  
 FT Protein 17..161 /label= Mature\_IL\_17L\_protein  
 XX WO200208285-A2.  
 XX 31-JAN-2002.  
 XX 21-JUN-2001; 2001WO-US19861.  
 XX 22-JUN-2000; 2000US-213125P.  
 PR 02-FEB-2001; 2001US-266159P.  
 PR 16-MAR-2001; 2001US-0810384.  
 XX (AMGE-) AMGEN INC.  
 XX Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;  
 XX WPI; 2002-155217/20.  
 DR N-PSDB; AAD28771.  
 XX Nucleic acid molecules encoding Interleukin 17 (IL-17) - like  
 PT polypeptides useful in the treatment, prevention and diagnosis of  
 XX diseases e.g. cancer  
 PS Claim 13; Fig 1; 242pp; English.  
 XX The invention relates to nucleic acid molecules encoding Interleukin 17  
 CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
 CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,  
 CC preventing or ameliorating a disease, such as immune system dysfunction  
 CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);  
 CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel  
 CC disease, transplant rejection, graft vs. host disease); infections (HIV,  
 CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,  
 CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
 CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin  
 CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
 CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy  
 CC atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma  
 CC leukaemia); reproductive (infertility, miscarriage, endometriosis), eye  
 CC (blindness, retinal neuropathy) and treatment of diseases involving  
 CC inflammation. The present sequence is human Interleukin-17 like (IL-17L)  
 CC protein.  
 XX Sequence 161 AA;  
 SQ  
 Query Match 100.0%; Score 910; DB 23; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MYQVAFAMVWGTHYTHSWPSCCPKSGQDTSEELLRWSTVPVPPLEPARNRHPESCRA 60  
 DB 1 MYQVAFAMVWGTHYTHSWPSCCPKSGQDTSEELLRWSTVPVPPLEPARNRHPESCRA 60  
 QY 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLCPHCVSLOTGSHMDPRGNSSELYHN 120  
 DB 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLCPHCVSLOTGSHMDPRGNSSELYHN 120  
 QY 121 QTVFYRRCPCHGKGTGKCYCLERRLYRVSLACVCRVRVMG 161  
 DB 121 QTVFYRRCPCHGKGTGKCYCLERRLYRVSLACVCRVRVMG 161  
 RESULT 4  
 ID AAM52691 standard; Protein; 161 AA.  
 XX AAM52691;  
 XX 26-FEB-2002 (first entry)  
 XX



DE Human interleukin 174 (IL-174).  
 XX Human; interleukin 174; IL-174; cytokine; Th2 response;  
 KW innate immune response; inflammation; gut cell growth;  
 KW extramedullary haematopoiesis; antibody response; granuloma formation;  
 KW autoimmune condition; multiple sclerosis; systemic lupus erythematosus;  
 KW rheumatoid arthritis; diabetes; psoriasis; infectious agent;  
 KW inflammatory condition; Crohn's disease; ulcerative colitis;  
 KW pancreatitis; hepatitis; allergy; Th2-mediated condition;  
 KW systemic anaphylactic response; skin hypersensitivity response;  
 KW dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator;  
 KW antiinflammatory; antiarthritic; antidiabetic; antifungal;  
 KW dermatological; neuroprotective; antiallergic; agonist; antagonist.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..16  
 FT /label= Signal\_peptide  
 FT Protein 17..161  
 FT /label= Mature\_IL-174  
 XX  
 XX WO200179288-A2.  
 XX  
 XX 25-OCT-2001.  
 XX  
 XX 17-APR-2001; 2001WO-US12493.  
 XX  
 XX 18-APR-2000; 2000US-198488P.  
 XX  
 XX (SCHE ) SCHERING CORP.  
 XX  
 XX Hurst SD, Zurawski SM, Rennick DM;  
 XX  
 XX WPI; 2002-034343/04.  
 XX N-PSDB; ABA02393.  
 XX  
 XX Administering an interleukin 174 agonist or antagonist to a mammal  
 XX regulates various immune and inflammatory responses and is useful to  
 XX treat for example autoimmune diseases, allergies or response to an  
 XX infection -  
 XX  
 XX Examples; Page 27-28; 29pp; English.  
 XX  
 XX The invention relates to methods of directing an immune response in a  
 XX mammal by the administration of an agonist or antagonist of the cytokine  
 XX interleukin 174 (IL-174). Administration of an IL-174 agonist directs the  
 XX immune response towards a Th2 response, stimulates an innate immune  
 XX response, augments the inflammatory response from epithelial or  
 XX fibroblast cells, induces gut cell growth, promotes extramedullary  
 XX haematopoiesis, or augments an antibody response in serum and faecal  
 XX material, while administration of an IL-174 antagonist directs the immune  
 XX response away from a Th2 type response, and prevents inflammation or  
 XX granuloma formation. IL-174 agonists may be used to treat autoimmune  
 XX conditions (particularly multiple sclerosis, systemic lupus  
 XX erythematosus, rheumatoid arthritis, diabetes or psoriasis), a response  
 XX to an infectious agent, or inflammatory conditions such as Crohn's  
 XX disease, ulcerative colitis, pancreatitis, or hepatitis. IL-174  
 XX antagonists may be used to treat inflammatory, allergic or Th2-mediated  
 XX conditions (e.g., systemic anaphylactic response, skin hypersensitivity  
 XX response, dermatitis, asthma, fibrosis, or eosinophilic gastritis). The  
 XX present sequence represents human IL-174.  
 XX  
 XX Sequence 161 AA;  
 XX  
 XX Query Match 100.0%; Score 910; DB 23; Length 161;  
 XX Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
 XX Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYQVAFAMVNGTHTYSHNPPSCPSKQDTSEELLRWSTVPVPLEPARNRHPESCRA 60  
 DB 1 MYQVAFAMVNGTHTYSHNPPSCPSKQDTSEELLRWSTVPVPLEPARNRHPESCRA 60

Oy 61 SEDGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDPRGNSELLYHN 120  
 Db 61 SEDGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDPRGNSELLYHN 120  
 Oy 121 QTVFYRRPCHGKGTGKGLRRLRYRSLACVCRPRVMG 161  
 Db 121 QTVFYRRPCHGKGTGKGLRRLRYRSLACVCRPRVMG 161  
 RESULT 5  
 AAM47464  
 ID AAM47464 standard; Protein; 161 AA.  
 XX  
 AC AAM47464;  
 XX  
 XX 11-FEB-2002 (first entry)  
 XX  
 DE Human IL-17 receptor like protein ligand, IL-17E.  
 XX  
 XX Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic;  
 KW antipsoriatic; antimicrobial; anorectic; nootropic; neuroprotective;  
 KW antichlamic; antiallergic; dermatological; cytostatic; gene therapy;  
 KW interleukin 17; immune system disorder; infection; weight; reproductive;  
 KW neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation;  
 KW glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;  
 KW tumour; IL-17E.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200168705-A2.  
 PN  
 XX 20-SEP-2001.  
 PD  
 XX  
 PF 16-MAR-2001; 2001WO-US08688.  
 XX  
 XX 16-MAR-2000; 2000US-189923P.  
 PR  
 XX 12-MAY-2000; 2000US-204208P.  
 PR  
 XX 27-NOV-2000; 2000US-072322.  
 PR  
 XX 02-FEB-2001; 2001US-266159P.  
 PA (AMGE-) AMGEN INC.  
 XX  
 XX Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ;  
 PI  
 XX WPI; 2002-055100/07.  
 DR N-PSDB; ABA03213.  
 XX  
 XX Three human nucleic acids encoding interleukin 17 (IL-17) receptor like  
 XX polypeptides, useful for treating, diagnosing, ameliorating or  
 XX preventing immune system disorders (e.g. psoriatic arthritis) and  
 XX infections (e.g. viral infections) -  
 XX  
 XX Example 7; Page 234-235; 239pp; English.  
 XX  
 XX The present invention relates to novel human nucleic acids encoding  
 XX interleukin 17 (IL-17) receptor like proteins (see ABA03200-ABA03202,  
 XX AAM47456, AAM47458 and AAM47459). The IL-17 receptor-like proteins and  
 XX coding sequences are useful for treating a pathological condition related  
 XX to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.  
 XX viral infections), weight disorders (e.g. obesity), neuronal dysfunction  
 XX disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin  
 XX disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),  
 XX bone disease (e.g. osteoporosis), vascular system disorders (e.g.  
 XX ischaemia), eye disorders, reproductive disorders, tumours and  
 XX inflammation. The present sequence is the protein sequence for IL-17E, a  
 XX human IL-17 receptor like protein ligand.  
 XX  
 XX Sequence 161 AA;  
 XX  
 XX Query Match 100.0%; Score 910; DB 23; Length 161;  
 XX Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
 XX Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYQVAFAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPPLEPARPNRHPSRCRA 60  
 Db 1 MYQVAFAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPPLEPARPNRHPSRCRA 60  
 QY 61 SEDGPLNSRAISPRWYELDRDLNRLPQDLYHARCLCPHCYSLQTSQSHMDPRGNSSELLYHN 120  
 Db 61 SEDGPLNSRAISPRWYELDRDLNRLPQDLYHARCLCPHCYSLQTSQSHMDPRGNSSELLYHN 120  
 QY 121 QTVFYRRPCHGKGTHTKGYCLERRLYRVSLACVVCVRPVWG 161  
 Db 121 QTVFYRRPCHGKGTHTKGYCLERRLYRVSLACVVCVRPVWG 161  
 RESULT 6  
 ID AAU04952  
 AC AAU04952 standard; Protein; 177 AA.  
 AC AAU04952;  
 XX 24-OCT-2001 (first entry)  
 XX Human Interleukin 17E ligand, IL-17E.  
 XX Human; Interleukin-17E ligand; IL-17E; agonist; antagonist;  
 KW PRO10272; DNA 147531-2821; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;  
 KW allergic disease; asthma; demyelinating disease;  
 KW degenerative cartilaginous disorder; transplantation associated disease.  
 XX Homo sapiens.  
 XX Key  
 FH Peptide  
 FT 1..32 Location/Qualifiers  
 FT /label= Signal\_peptide  
 FT Protein 33..177  
 FT /label= Mature\_IL\_17E  
 FT Region 44..50  
 FT /note= "N-myristoylation site"  
 FT Region 127..135  
 FT /note= "Tyrosine kinase phosphorylation site"  
 FT Modified-site 136..140  
 FT /note= "Asn is glycosylated"  
 FT Region 150..156  
 FT /note= "N-myristoylation site"  
 XX WO200146420-A2.  
 XX 28-JUN-2001.  
 XX 20-DEC-2000; 2000WO-US34956.  
 XX 23-DEC-1999; 99US-0172096.  
 XX 30-DEC-1999; 99WO-US31274.  
 XX 11-JAN-2000; 2000US-0175481.  
 XX 18-FEB-2000; 2000WO-US04341.  
 XX 02-MAR-2000; 2000WO-US05841.  
 XX 21-MAR-2000; 2000US-0191007.  
 XX 21-MAR-2000; 2000WO-US07532.  
 XX 02-JUN-2000; 2000WO-US5264.  
 XX 22-JUN-2000; 2000US-0213087.  
 XX 24-AUG-2000; 2000US-0644848.  
 XX 24-AUG-2000; 2000WO-US23328.  
 XX 24-OCT-2000; 2000US-0242837.  
 XX 10-NOV-2000; 2000WO-US08073.  
 XX 28-NOV-2000; 2000US-0235646.  
 XX 01-DEC-2000; 2000WO-US32678.  
 XX (GETH ) GENENTECH INC.  
 XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;  
 PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL;  
 PI Watanabe CK, Williams PM, Wood WI, Yansura DG;

DR WPI; 2001-451708/48.  
 XX N-PSDB; AAS09511.  
 XX Novel PRO polypeptides homologous to interleukin-17, useful for the  
 PT diagnosis and treatment of immune related disease e.g. rheumatoid  
 PT arthritis and diabetes  
 XX Claim 10; Fig 6; 188pp; English.  
 XX The sequence is PRO10272 which is the human Interleukin 17E ligand,  
 CC IL-17E, encoded by DNA 147531-2821. A composition  
 CC containing ant/agonists to the PRO polypeptides or individual components  
 CC are useful for treating a mammal with an immune related disease, e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune renal  
 CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated skin  
 CC disease, contact dermatitis, an allergic disease e.g. food  
 CC hypersensitivity, asthma, a transplantation associated disease, or a  
 CC chronic inflammatory demyelinating polyneuropathy. Treating a  
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or  
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous  
 CC examples of the diseases and disorders are given in the specification.  
 XX Sequence 177 AA;  
 SQ  
 Query Match 98.7%; Score 898; DB 22; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-85;  
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QVVAFLAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPPLEPARPNRHPSRCRA 62  
 Db 19 QVVAFLAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPPLEPARPNRHPSRCRA 78  
 QY 63 DGPLNSRAISPRWYELDRDLNRLPQDLYHARCLCPHCYSLQTSQSHMDPRGNSSELLYHNQT 122  
 Db 79 DGPLNSRAISPRWYELDRDLNRLPQDLYHARCLCPHCYSLQTSQSHMDPRGNSSELLYHNQT 138  
 QY 123 VFYRRPCHGKGTHTKGYCLERRLYRVSLACVVCVRPVWG 161  
 Db 139 VFYRRPCHGKGTHTKGYCLERRLYRVSLACVVCVRPVWG 177  
 RESULT 7  
 AAB47299  
 ID AAB47299 standard; Protein; 177 AA.  
 XX AAB47299;  
 XX 22-AUG-2001 (first entry)  
 XX PRO10272 polypeptide.  
 XX PRO; PRO1081; PRO1274; PRO10272; proliferation; T-lymphocyte;  
 KW PRO1199; PRO1556; PRO4401; PRO10268; inhibition; stimulation;  
 KW infiltration; mononuclear cell; eosinophil; erythema multiforme;  
 KW polymorphonuclear neutrophil; PMN; antibody; immune-related disorder;  
 KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;  
 KW juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; skin disease;  
 KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anemia; asthma;  
 KW autoimmune thrombocytopaenia; thyroiditis; diabetes mellitus; allergy;  
 KW immune-mediated renal disease; demyelination; central nervous system;  
 KW peripheral nervous system; idiopathic demyelinating polyneuropathy;  
 KW Guillain-Barre syndrome; hepatobiliary disease; eosinophilic pneumonia;  
 KW chronic active hepatitis; primary biliary cirrhosis; allergic rhinitis;  
 KW granulomatous hepatitis; sclerosing cholangitis; food hypersensitivity;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy; urticaria;  
 KW Whipple's disease; idiopathic pulmonary fibrosis; contact dermatitis;  
 KW psoriasis; atopic dermatitis; hypersensitivity pneumonitis;  
 KW graft rejection; graft-versus-host disease.

XX OS Homo sapiens.

XX FH Key

XX FT Peptide

XX FT Protein

XX FT Modified-site

XX FT Modified-site

XX FT Modified-site

XX FT Modified-site

XX FT Modified-site

XX FT Modified-site

XX PN WO200140465-A2.

XX PN 07-JUN-2001.

XX PF 10-NOV-2000; 2000WO-US30873.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 09-DEC-1999; 99US-0170262.

XX PR 23-DEC-1999; 99US-0172059.

XX PR 11-JAN-2000; 2000US-0175481.

XX PR 20-JAN-2000; 2000US-0177118.

XX PR 18-FEB-2000; 2000WO-US04342.

XX PR 03-MAR-2000; 2000US-0187202.

XX PR 30-MAY-2000; 2000WO-US14941.

XX PR 05-JUN-2000; 2000US-0209832.

XX PR 24-AUG-2000; 2000WO-US23328.

XX PA (GETH ) GENENTECH INC.

XX PI Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

XX PI Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX DR N-PSDB; AAC85969.

XX DR WPI; 2001-381384/40.

XX PS Isolated PRO polypeptide useful for treat or diagnose an immune-related disorder e.g. arthritis, asthma, allergy, diabetes or psoriasis -

XX PS Claim 1; Fig 18; 124pp; English.

XX CC The sequences given in AAB47291-99 show PRO polypeptides. PRO1081, PRO1274 and PRO10272 stimulate the proliferation of T-lymphocytes and PRO1199, PRO1556, PRO4401 and PRO10268 inhibit the proliferation of T-lymphocytes. PRO1754 and PRO9912 act to enhance the infiltration of mononuclear cells, eosinophils or polymorphonuclear neutrophils (PMN) into the tissue of a mammal. The PRO cDNA's and antibodies which bind to them, are used to treat an immune-related disorder in a mammal. Such disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic inflammatory demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease.

XX SQ Sequence 177 AA:

XX SQ Query Match

XX SQ Best Local Similarity 100.0%; Pred. No. 8.1e-85;

XX SQ Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 3 QVVAFLAMVGMTHYSHWPSCCPKSGQDTSEELLRWSTVPVPPLEPARNRHPSERASE 62

XX DB 19 QVVAFLAMVGMTHYSHWPSCCPKSGQDTSEELLRWSTVPVPPLEPARNRHPSERASE 78

XX QY 63 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCICPHCVSLQTSQSHMDPRGNSSELLYHNQT 122

XX DB 79 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCICPHCVSLQTSQSHMDPRGNSSELLYHNQT 138

XX QY 123 VFYRRPCHGKTHGKCYCLERRLYRVSLACVYVPRVMG 161

XX DB 139 VFYRRPCHGKTHGKCYCLERRLYRVSLACVYVPRVMG 177

XX RESULT 8

XX AAB87603

XX ID AAB87603 standard; Protein; 177 AA.

XX AC AAB87603;

XX XX

XX DT 15-MAY-2001 (first entry)

XX DE Human PRO10272.

XX XX

XX KW Human; PRO protein; mapping.

XX XX

XX OS Homo sapiens.

XX XX

XX PN WO200116318-A2.

XX PD 08-MAR-2001.

XX XX

XX PF 24-AUG-2000; 2000WO-US23328.

XX PR 01-SEP-1999; 99WO-US20111.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 07-DEC-1999; 99US-0169495.

XX PR 09-DEC-1999; 99US-0170262.

XX PR 11-JAN-2000; 2000US-0175481.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 18-FEB-2000; 2000WO-US04342.

XX PR 22-FEB-2000; 2000WO-US04414.

XX PR 01-MAR-2000; 2000WO-US05601.

XX PR 03-MAR-2000; 2000US-0187202.

XX PR 25-APR-2000; 2000US-0199397.

XX PR 22-MAY-2000; 2000WO-US14042.

XX PR 05-JUN-2000; 2000US-0209832.

XX XX

XX PA (GETH ) GENENTECH INC.

XX PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

XX PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

XX XX

XX DR WPI; 2001-183260/18.

XX DR N-PSDB; AAF92135.

XX XX

XX PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.

XX PT Claim 12; Fig 156; 278pp; English.

XX PS

XX CC The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be

CC employed as molecular weight markers for protein electrophoresis. The PRO  
CC coding sequence has applications in molecular biology, including use as  
CC hybridisation probes, and in chromosome and gene mapping.  
XX  
SQ Sequence 177 AA;

Query Match 98.7%; Score 898; DB 22; Length 177;  
Best Local Similarity 100.0%; Pred. No. 8.1e-85;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QVAFVAMVMTHTYSHWPCSCPSKQDTSSELLRWSTVPVPPLEPARNRHPESCRASE 62  
Db 19 QVAFVAMVMTHTYSHWPCSCPSKQDTSSELLRWSTVPVPPLEPARNRHPESCRASE 78  
QY 63 DGPLNSRAISPRYELDRDLNLPQDLYHARCLCHVCVSLQTGSHMDPRGNSSELLYHNOT 122  
Db 79 DGPLNSRAISPRYELDRDLNLPQDLYHARCLCHVCVSLQTGSHMDPRGNSSELLYHNOT 138  
QY 123 VFYRPPCHGEKTHGKGYCLERRLRYSLACVCRPRVMG 161  
Db 139 VFYRPPCHGEKTHGKGYCLERRLRYSLACVCRPRVMG 177

RESULT 9  
ABG29372  
ID ABG29372 standard; Protein; 350 AA.  
XX  
AC ABG29372;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #29363.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US08631.  
XX  
XX 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI: 2001-639362/73.  
DR N-PSDB; AAS93559.  
XX

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity  
XX  
PS Claim 20; SEQ ID No 59731; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human  
...CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 350 AA;

Query Match 91.6%; Score 834; DB 22; Length 350;  
Best Local Similarity 91.1%; Pred. No. 7.8e-78;  
Matches 153; Conservative 1; Mismatches 4; Indels 10; Gaps 2;

QY 3 QVAFVAMVMTHTYSHWPCSCPSKQDTSSELLRWSTVPVPPLEPARNRHPESCRASE 62  
Db 28 RVVAFVAMVMTHTYSHWPCSCPSKQDTSSELLRWSTVPVPPLEPARNRHPESCRASE 87  
QY 63 DGPLNSRAISPRYELDRDLNLPQDLYHARCLCHVCVSLQTGSHMDPRGNS 114  
Db 88 DGPLNSRAISPRYELDRDLNLPQDLYHARCLCHVCVSLQTGSHMDPRGNS 147  
QY 115 ELLYHNQTVFYRPPCHGEKTHGKGYCLERRLRYSLACVCRPRVM 160  
Db 148 ELLYHNQTVFYRPPCHGEKTHGKGYCLERRLRYSLACVCRPRVM 195

RESULT 10  
AAB07600  
ID AAB07600 standard; Protein; 169 AA.  
XX  
AC AAB07600;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE A murine interleukin (IL) 174 polypeptide.  
XX  
KW Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;  
KW IL-177; IL-171; cell proliferation; cancer.  
XX  
OS Mus sp.

XX  
FH Key Location/Qualifiers  
FT Peptide 1..16 /note= "signal peptide"  
FT Modified-site 2..4 /note= "protein kinase C phosphorylation site"  
FT Protein 17..169 /note= "mature protein"  
FT Modified-site 18..20 /note= "calcium phosphorylation site"  
FT Modified-site 29..32 /note= "CAMP protein kinase phosphorylation site"  
FT Modified-site 29 /note= "phosphorylation site"  
FT Modified-site 31 /note= "phosphorylation site"  
FT Modified-site 49..51 /note= "protein kinase C phosphorylation site"  
FT Modified-site 51 /note= "phosphorylation site"  
FT Modified-site 53 /note= "phosphorylation site"  
FT Modified-site 53..55 /note= "calcium phosphorylation site"  
FT Modified-site 61 /note= "phosphorylation site"  
FT Modified-site 61..64 /note= "CAMP protein kinase phosphorylation site"  
FT Modified-site 64 /note= "phosphorylation site"

FT Modified-site 67..69 /note= "calcium phosphorylation site"  
FT Modified-site 112..114 /note= "N-glycosylation site"  
FT Modified-site 123..127 /note= "myristoylation site"  
FT Modified-site 127..129 /note= "protein kinase C phosphorylation site"  
FT Modified-site 139 /note= "phosphorylation site"  
FT Modified-site 141 /note= "phosphorylation site"  
XX WO200042188-A2.  
XX 20-JUL-2000.  
XX 10-JAN-2000; 2000WO-US000006.  
XX 11-JAN-1999; 99US-0228822.  
XX (SCHE ) SCHERING CORP.  
XX Gorman DM, Bazan JF, Kastelein RA;  
XX WPI; 2000-460130/40.  
XX N-PSDB; AAA58988.  
XX New isolated polynucleotide encoding a mammalian Interleukin-17 like  
XX protein used to identify genes for homologous proteins -  
XX Claim 11; Page 18; 11lpp; English.  
XX The present sequence represents an interleukin-174 (IL-174) polypeptide.  
XX The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a  
XX member of a new group of interleukins, IL-170 polypeptides. The members  
XX comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170  
XX protein can be used to treat abnormal proliferation e.g. cancer  
XX or degenerative conditions. Antibodies can be used in diagnostic  
XX methods to detect over production of IL-170 protein in cells or body  
XX fluids.  
XX Sequence 169 AA;  
Query Match 77.9%; Score 709; DB 21; Length 169;  
Best Local Similarity 76.8%; Pred. No. 2.7e-65;  
Matches 129; Conservative 9; Mismatches 22; Indels 8; Gaps 1;  
Qy 1 MYQVAFAMVNGTHY-----SHWPCCPSKQDTSPELLRWSTVPVPPLEPARPN 52  
Db 1 MYQVAFAMVNGTHY-----SHWPCCPSKQDTSPELLRWSTVPVPPLEPARPN 52  
Qy 53 RHPESCRASEDGLNSRAISRWYELDLNPLPDLYHARCLCPHCYSLOTGSHMDPRG 112  
Db 61 HHAESCRASKDGLNSRAISRWYELDLNPLPDLYHARCLCPHCYSLOTGSHMDPLG 120  
Qy 113 NSELYHNQTVFYRRPCHGEGTHKGYCLERRLYRVSLACVCRPRVM 160  
Db 121 NSVPLYHNQTVFYRRPCHGEGTHKGYCLERRLYRVSLACVCRPRVM 168  
RESULT 11  
AAB07694  
ID AAB07694 standard; Protein; 169 AA.  
AC AAB07694;  
XX 07-NOV-2000 (first entry)  
XX A murine interleukin-174 polypeptide.  
XX Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;  
KW IL-174; IL-176; IL-177; cell proliferation; cancer.

XX Mus sp.  
OS Key Location/Qualifiers  
XX Peptide 1..16 "signal peptide"  
FT Modified-site 2..4 /note= "protein kinase C phosphorylation site"  
FT Protein 17..169 /note= "mature protein"  
FT Modified-site 18..20 /note= "calcium phosphorylation site"  
FT Modified-site 29..32 /note= "cAMP protein kinase phosphorylation site"  
FT Modified-site 29 /note= "phosphorylation site"  
FT Modified-site 31 /note= "phosphorylation site"  
FT Modified-site 49..51 /note= "protein kinase C phosphorylation site"  
FT Modified-site 51 /note= "phosphorylation site"  
FT Modified-site 53 /note= "phosphorylation site"  
FT Modified-site 53..55 /note= "calcium phosphorylation site"  
FT Modified-site 61 /note= "phosphorylation site"  
FT Modified-site 61..64 /note= "cAMP protein kinase phosphorylation site"  
FT Modified-site 64 /note= "phosphorylation site"  
FT Modified-site 67..69 /note= "calcium phosphorylation site"  
FT Modified-site 112..114 /note= "N-glycosylation site"  
FT Modified-site 123..127 /note= "myristoylation site"  
FT Modified-site 127..129 /note= "protein kinase C phosphorylation site"  
FT Modified-site 139 /note= "phosphorylation site"  
FT Modified-site 141 /note= "phosphorylation site"  
FT WO200042187-A1.  
XX 20-JUL-2000.  
XX 10-JAN-2000; 2000WO-US000005.  
XX 11-JAN-1999; 99US-0229402.  
XX (SCHE ) SCHERING CORP.  
XX Gorman DM, Bazan JF, Kastelein RA;  
XX WPI; 2000-476060/41.  
XX N-PSDB; AAA59160.  
XX New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
XX interleukin-171 (IL-171), useful for recombinant production of IL-171  
XX which can be used for treating conditions associated with abnormal  
XX physiology or development -  
XX Disclosure; Page 21; 11lpp; English.  
XX The present sequence represents an interleukin (IL)-174 polypeptide.  
XX It is a mammalian homologue of the cytokine designated CTLA-8 (also  
XX referred to as IL-17). The specification also describes homologues  
XX IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
XX sequence encoding IL-171 is useful for identifying genes, mRNA and  
XX cDNA molecules which code for related or homologous proteins. The

CC IL-171 protein, antibodies against IL-171, and compounds which have  
 CC binding affinity to IL-171 are useful in treatment of conditions  
 CC associated with abnormal physiology or development, including abnormal  
 CC proliferation, e.g. cancerous conditions, or degenerative conditions.  
 CC The IL-171 protein can be used in kits and assay methods for identifying  
 CC compounds that selectively bind to IL-171.

SX Sequence 169 AA;  
 Query Match 77.9%; Score 709; DB 21; Length 169;  
 Best Local Similarity 76.8%; Pred. No. 2.7e-65;  
 Matches 129; Conservative 9; Mismatches 22; Indels 8; Gaps 1;  
 QY 1 MYQVAFAMVGMTHY-----SHWSPCCPSKGGDTSEELLRWSTVPPPLEPARPN 52  
 DB 1 MYQVAFAMVGMTHYVSLRIQEGCSHLPSCCPSKKEPPEEWLKWSSASVSPPELSHT 60  
 QY 53 RHPECRASEDGPLNSRAISPWRYELDRNLRLPQDLYHARCLCPHCVSLQTSMDPRG 112  
 DB 61 HHAESCRASKDGPLNSRAISPWRYELDRNLRLPQDLYHARCLCPHCVSLQTSMDPLG 120  
 QY 113 NSELLYHNOTVYRRPCHGKGTGKGYCLERLRYRSLACVCRPRYM 160  
 DB 121 NSVPLYHNOTVYRRPCHGEGTHRRYCLERLRYRSLACVCRPRYM 168

RESULT 12  
 AAE18121  
 ID AAE18121 standard; Protein; 169 AA.

XX AAE18121;  
 AC AAE18121;  
 DT 07-MAY-2002 (first entry)  
 DE Mouse Interleukin-17 like (IL-17L) protein.

KW Mouse; Interleukin-17 like; IL-17L; Immune system dysfunction; diabetes;  
 KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;  
 KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;  
 KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;  
 KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
 KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
 KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
 KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
 KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
 KW cancer.

XX Mus musculus.

OS  
 FH Key Location/Qualifiers  
 FT Peptide 1..18  
 FT Protein 19..169  
 FT /label= Signal\_peptide  
 FT /label= Mature\_IL\_17L\_protein

PN WO200208285-A2.

XX 31-JAN-2002.

XX 21-JUN-2001; 2001WO-US19861.

XX 22-JUN-2000; 2000US-213125P.

PR 02-FEB-2001; 2001US-266159P.

PR 16-MAR-2001; 2001US-081038A.

XX (AMGE-) AMGEN INC.

XX Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;

XX WPI; 2002-155217/20.

DR N-PSDB; AAD28772.

XX Nucleic acid molecules encoding Interleukin 17 (IL-17) - like

PT polypeptides useful in the treatment, prevention and diagnosis of  
 PT diseases e.g. cancer -

XX Claim 13; Fig 2; 242pp; English.

XX The invention relates to nucleic acid molecules encoding Interleukin 17  
 CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
 CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,  
 CC preventing or ameliorating a disease, such as immune system dysfunction  
 CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);  
 CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel  
 CC disease, transplant rejection, graft vs. host disease); infections (HIV,  
 CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,  
 CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
 CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin  
 CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
 CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy  
 CC atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma  
 CC leukaemia); reproductive (infertility, miscarriage, endometriosis), eye  
 CC (blindness), retinal neuropathy) and treatment of diseases involving  
 CC inflammation. The present sequence is mouse Interleukin-17 like (IL-17L)  
 CC protein.

XX Sequence 169 AA;

Query Match 77.9%; Score 709; DB 23; Length 169;  
 Best Local Similarity 76.8%; Pred. No. 2.7e-65;  
 Matches 129; Conservative 9; Mismatches 22; Indels 8; Gaps 1;

QY 1 MYQVAFAMVGMTHY-----SHWSPCCPSKGGDTSEELLRWSTVPPPLEPARPN 52  
 DB 1 MYQVAFAMVGMTHYVSLRIQEGCSHLPSCCPSKKEPPEEWLKWSSASVSPPELSHT 60  
 QY 53 RHPECRASEDGPLNSRAISPWRYELDRNLRLPQDLYHARCLCPHCVSLQTSMDPRG 112  
 DB 61 HHAESCRASKDGPLNSRAISPWRYELDRNLRLPQDLYHARCLCPHCVSLQTSMDPLG 120  
 QY 113 NSELLYHNOTVYRRPCHGKGTGKGYCLERLRYRSLACVCRPRYM 160  
 DB 121 NSVPLYHNOTVYRRPCHGEGTHRRYCLERLRYRSLACVCRPRYM 168

RESULT 13

AA52692

ID AA52692 standard; Protein; 169 AA.

XX AA52692;

DT 26-FEB-2002 (first entry)

DE Murine interleukin 174 (IL-174).

KW Mouse; murine; interleukin 174; IL-174; cytokine; Th2 response;  
 KW innate immune response; inflammation; gut cell growth;  
 KW extramedullary haematopoiesis; antibody response; granuloma formation;  
 KW autoimmune condition; multiple sclerosis; systemic lupus erythematosus;  
 KW rheumatoid arthritis; diabetes; psoriasis; infectious agent;  
 KW inflammatory condition; Crohn's disease; ulcerative colitis;  
 KW pancreatitis; hepatitis; allergy; Th2-mediated condition;  
 KW systemic anaphylactic response; skin hypersensitivity response;  
 KW dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator;  
 KW antiinflammatory; antiarthritic; antidiabetic; antifungal;  
 KW dermatological; neuroprotective; antiallergic; agonist; antagonist.

XX Mus sp.

XX Key Location/Qualifiers  
 FH Peptide 1..16  
 FT Protein 17..169  
 FT /label= Signal\_peptide  
 FT /label= Mature\_IL-174

XX WO200179288-A2.

XX PD 25-OCT-2001.  
XX PF 17-APR-2001; 2001WO-US12493.  
XX PR 18-APR-2000; 2000US-198488P.  
XX PA (SCHE) SCHERING CORP.  
XX PI Hurst SD, Zurawski SM, Rennick DM;  
XX DR WPI; 2002-034343/04.  
XX DR N-PSDB; ABA02394.  
XX PT Administering an interleukin 174 agonist or antagonist to a mammal  
XX PT regulates various immune and inflammatory responses and is useful to  
XX PT treat for example autoimmune diseases, allergies or response to an  
XX PS infection  
XX PS Examples; Page 29; 29pp; English.  
XX CC The invention relates to methods of directing an immune response in a  
XX CC mammal by the administration of an agonist or antagonist of the cytokine  
XX CC interleukin 174 (IL-174). Administration of an IL-174 agonist directs the  
XX CC immune response towards a Th2 response, stimulates an innate immune  
XX CC response, augments the inflammatory response from epithelial or  
XX CC fibroblast cells, induces gut cell growth, promotes extramedullary  
XX CC haematopoiesis, or augments an antibody response in serum and faecal  
XX CC material, while administration of an IL-174 antagonist directs the immune  
XX CC response away from a Th2 type response, and prevents inflammation or  
XX CC granuloma formation. IL-174 agonists may be used to treat autoimmune  
XX CC conditions (particularly multiple sclerosis, systemic lupus  
XX CC erythematosus, rheumatoid arthritis, diabetes or psoriasis), a response  
XX CC to an infectious agent, or inflammatory conditions such as Crohn's  
XX CC disease, ulcerative colitis, pancreatitis, or hepatitis. IL-174  
XX CC antagonists may be used to treat inflammatory, allergic or Th2-mediated  
XX CC conditions (e.g., systemic anaphylactic response, skin hypersensitivity  
XX CC response, dermatitis, asthma, fibrosis, or eosinophilic gastritis). The  
XX CC present sequence represents murine IL-174.  
XX CC Sequence 169 AA;  
Query Match 77.9%; Score 709; DB 23; Length 169;  
Best Local Similarity 76.8%; Pred. No. 2.7e-65;  
Matches 129; Conservative 9; Mismatches 22; Indels 8; Gaps 1;  
QY 1 MYQVAVFLAMVGTHTY-----SHWPCCPCKSGQDTSEELLRWSTVPPLEPARN 52  
DB 1 MYQVAVFLAMVGTHTVSLRIGCGSHLPSCCPCKSEKEPPEEWLKWSSASVSPPEPLSHT 60  
QY 53 RHPECSRASEDGPLNSRAISPMRYELDRDLNRLPDQLYHARCLPCHVSLQGTGSHMDPRG 112  
DB 61 HHAESCRASKDGPLNSRAISPMRYELDRDLNRLPDQLYHARCLPCHVSLQGTGSHMDPLG 120  
QY 113 NSLEYLHNQTVFRRPCHGEKTHGYCLERLRYVSLACVCRPRVM 160  
DB 121 NSVPLYHNQTVFRRPCHGEKTHGYCLERLRYVSLACVCRPRVM 168  
RESULT 14  
AAE18122  
ID AAE18122 standard; Protein: 160 AA.  
XX AC AAE18122;  
XX DT 07-MAY-2002 (first entry)  
XX DE Mouse non-secreted form of Interleukin-17 like (IL-17L) protein.  
XX KW Mouse; interleukin-17 like; IL-17L; immune system dysfunction; diabetes;  
XX KW cystostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;  
XX KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;  
XX KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;

KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
XX cancer.  
XX OS Mus musculus.  
XX PN WO200208285-A2.  
XX PD 31-JAN-2002.  
XX PF 21-JUN-2001; 2001WO-US19861.  
XX PR 22-JUN-2000; 2000US-213125P.  
XX PR 02-FEB-2001; 2001US-266159P.  
XX PR 16-MAR-2001; 2001US-0810384.  
XX PA (AMGE-) AMGEN INC.  
XX PI Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HO, Jing S;  
XX WPI; 2002-155217/20.  
XX DR N-PSDB; AAD28773.  
XX PT Nucleic acid molecules encoding Interleukin 17 (IL-17) - like  
XX PT polypeptides useful in the treatment, prevention and diagnosis of  
XX PT diseases e.g. cancer  
XX PS Claim 13; Fig 2; 242pp; English.  
XX CC The invention relates to nucleic acid molecules encoding Interleukin 17  
XX CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
XX CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,  
XX CC preventing or ameliorating a disease, such as immune system dysfunction  
XX CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);  
XX CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel  
XX CC disease, transplant rejection, graft vs. host disease); infections (HIV,  
XX CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,  
XX CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
XX CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin  
XX CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
XX CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy  
XX CC atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma  
XX CC leukaemia); reproductive (infertility, miscarriage, endometriosis), eye  
XX CC (blindness, retinal neuropathy) and treatment of diseases involving  
XX CC inflammation. The present sequence is non-secreted form of mouse  
XX CC Interleukin-17 like (IL-17L) cDNA.  
XX CC Note: The present sequence also shown in sequence listing of the  
XX CC specification lacks a residue at the C terminal end.  
XX CC Sequence 160 AA;  
Query Match 73.6%; Score 670; DB 23; Length 160;  
Best Local Similarity 76.1%; Pred. No. 2.7e-61;  
Matches 121; Conservative 9; Mismatches 21; Indels 8; Gaps 1;  
QY 10 MYVGTHTY-----SHWPCCPCKSGQDTSEELLRWSTVPPLEPARNHPESCAS 61  
DB 1 MYVGTHTVSLRIGCGSHLPSCCPCKSEKEPPEEWLKWSSASVSPPEPLSTHTHAESCRAS 60  
QY 62 EDGPLNSRAISPMRYELDRDLNRLPDQLYHARCLPCHVSLQGTGSHMDPRGNSLEYLHNQ 121  
DB 61 KDGPLNSRAISPMRYELDRDLNRLPDQLYHARCLPCHVSLQGTGSHMDPLGNSVPLYHNQ 120  
QY 122 TVFRRPCHGEKTHGYCLERLRYVSLACVCRPRVM 160  
DB 121 TVFRRPCHGEKTHGYCLERLRYVSLACVCRPRVM 159  
RESULT 15  
AAB07599



Query Match 38.6%; Score 351.5; DB 21; Length 144;  
Best Local Similarity 59.8%; Pred. No. 2e-28;  
Matches 70; Conservative 6; Mismatches 36; Indels 5; Gaps 2;

Search completed: May 12, 2003, 01:59:02  
Job time : 45 secs

GenCore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 00:49:29 ; Search time 1520 Seconds  
(without alignments)  
12330.399 Million cell updates/sec

Title: US-10-037-591A-1  
Perfect score: 644  
Sequence: 1 ctcaagtcactccctcaaaaa.....ggccccgtgtgatggctag 644

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	644	100.0	644	6	AX253225	Sequence
2	644	100.0	644	6	AX365242	Sequence
3	493	76.6	504	6	AX299773	Sequence
4	478.4	74.3	1320	6	AX092424	Sequence
5	478.4	74.3	1320	6	AX164145	Sequence
6	478.4	74.3	1320	6	AX180768	Sequence
7	478.4	74.3	1335	9	AF305200	AF305200 Homo sapi
8	478	74.2	486	9	AF458059	AF458059 Homo sapi
9	336.8	52.3	1013	6	AX365244	Sequence
10	336.2	52.2	1496	6	AX365250	Sequence
11	335.2	52.0	985	6	AX299775	Sequence
12	335.2	52.0	985	10	AF458060	AF458060 Mus muscu
13	327	50.8	462	10	AY034088	AY034088 Mus muscu
14	256	39.8	157910	9	CNS01DTR	AL132855 Human chr
15	256	39.8	196292	9	CNS0000B	AL049829 Human chr
16	196.8	30.6	145762	2	AC130940	AC130940 Rattus no
17	196.8	30.6	160950	2	AC119293	AC119293 Rattus no
18	140.2	21.8	170032	2	AC116673	AC116673 Mus muscu
19	121	18.8	160950	2	AC119293	AC119293 Rattus no
20	121	18.8	171821	2	AC115371	AC115371 Rattus no
21	53.8	8.4	591	6	AX427978	Sequence
22	53.8	8.4	1047	6	AX180766	Sequence
23	53.8	8.4	1047	6	AX376380	Sequence
24	53.8	8.4	1047	9	AF152099	AF152099 Homo sapi
25	53.8	8.4	1078	9	AF142410	AF142410 Homo sapi
26	53.8	8.4	1177	6	AX223949	Sequence
27	47.8	7.4	585	10	AF458061	AF458061 Mus muscu
28	47.6	7.4	125020	9	AF429315	AF429315 Homo sapi
29	45.8	7.1	214572	10	AL450341	AL450341 Mouse DNA
30	45	7.0	45	6	AX180787	Sequence
31	44.8	7.0	153500	2	AC128380	Sequence
32	43.6	6.8	125020	9	AF429315	AF429315 Homo sapi
33	42.8	6.6	183900	2	AC102499	AC102499 Mus muscu
34	42.4	6.6	241087	14	AF480884	AF480884 Chimpanze
35	42	6.5	10732	6	E32986	E32986 Gene encodi
36	41.8	6.5	92607	9	AL583807	AL583807 Human DNA
37	41.4	6.4	884	9	AF218727	AF218727 Homo sapi
38	41.4	6.4	687	6	AX047648	Sequence
39	41.4	6.4	687	6	AX055448	Sequence
40	41.4	6.4	687	6	AX180764	Sequence
41	41.4	6.4	687	6	AX464312	Sequence
42	41.4	6.4	687	9	AF152098	AF152098 Homo sapi
43	41.4	6.4	688	9	AF184969	AF184969 Homo sapi
44	41.4	6.4	703	9	AF110385	AF110385 Homo sapi
45	41.4	6.4	711	9	AF212311	AF212311 Homo sapi

ALIGNMENTS

RESULT 1  
AX253225  
LOCUS AX253225 644 bp DNA linear PAT 05-OCT-2001  
DEFINITION Sequence 22 from Patent WO0168705.  
ACCESSION AX253225  
VERSION AX253225.1 GI:15986362  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 644)  
AUTHORS Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and  
Nguyen,H.O.  
TITLE IL-17 receptor like molecules and uses thereof

JOURNAL Patent: WO 0168705-A 22 20-SEP-2001;  
Angen Inc. (US)

FEATURES

source Location/Qualifiers  
1. .644  
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/db\_xref="taxon:9606"  
159. .644  
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/db\_xref="GI:15986363"  
/translation="MYQVAFAMVMTHTYSHWPCPSKQDTSSELLRWSTVPVP  
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QTGSHMDPRGNSSELYHNQTVFYRRPCHGKGTGKGYCLERRLYRVSLACVCRPRYM  
G"  
BASE COUNT 144 a 204 c 173 g 123 t  
ORIGIN

Query Match 100.0%; Score 644; DB 6; Length 644;  
Best Local Similarity 100.0%; Pred. No. 6.3e-149;  
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTCAGTCACCTCCCTAAAGACAGTGGAAATAATTTGAATAACAACAGGCTTGTCT 60  
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Qy 61 GAAATAAATCAGGACTCCCTAACCTGCTCCAGTCAGCTCTTCCACAGGCTGTCTAG 120  
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Qy 121 TCAGTGGCCCCACTTGTGACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 180  
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Qy 181 TGGCAATGGTTCATGGGAACCCACACCTACAGCCAGTGGCCAGCTGTGCCCCAGCAAG 240  
Db 181 TGGCAATGGTTCATGGGAACCCACACCTACAGCCAGTGGCCAGCTGTGCCCCAGCAAG 240  
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Qy 421 ACCTGTACCGCCGCTGTGCTGTGCCCGCACTGGCTCAGCTACAGACAGGCTCCCAACA 480  
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Db 481 TGGACCCCGGGGCAACTCGGAGTGTCTTACCAACAACAGACTGTCTTACCGGGCGC 540  
Qy 541 CATGCCATGGCGAGAGGCAACCCACAGGCTACTGCTGAGCGGAGGCTGTACCCGTG 600  
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Qy 601 TTTCCTTAGCTTGTGTGTGTGGGCGCCCGTGTGATGGGCTAG 644  
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RESULT 2  
AX365242  
LOCUS AX365242 644 bp DNA linear PAT 15-FEB-2002  
DEFINITION Sequence 1 from Patent WO2002825.  
ACCESSION AX365242  
VERSION AX365242.1 GI:18696995

KEYWORDS  
SOURCE

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS  
Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S., Nguyen, H.O. and  
Jing, S.  
TITLE  
IL-17 molecules and uses thereof  
JOURNAL  
Patent: WO 0208285-A 1 31-JAN-2002;  
Angen, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1. .644  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
159. .644  
/note="unnamed protein product"  
/codon\_start=1  
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G"  
BASE COUNT 144 a 204 c 173 g 123 t  
ORIGIN

Query Match 100.0%; Score 644; DB 6; Length 644;  
Best Local Similarity 100.0%; Pred. No. 6.3e-149;  
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTCAGTCACCTCCCTAAAGACAGTGGAAATAATTTGAATAACAACAGGCTTGTCT 60  
Db 1 CTCAGTCACCTCCCTAAAGACAGTGGAAATAATTTGAATAACAACAGGCTTGTCT 60  
Qy 61 GAAATAAATCAGGACTCCCTAACCTGCTCCAGTCAGCTCTTCCACAGGCTGTCTAG 120  
Db 61 GAAATAAATCAGGACTCCCTAACCTGCTCCAGTCAGCTCTTCCACAGGCTGTCTAG 120  
Qy 121 TCAGTGGCCCCACTTGTGACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 180  
Db 121 TCAGTGGCCCCACTTGTGACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 180  
Qy 181 TGGCAATGGTTCATGGGAACCCACACCTACAGCCAGTGGCCAGCTGTGCCCCAGCAAG 240  
Db 181 TGGCAATGGTTCATGGGAACCCACACCTACAGCCAGTGGCCAGCTGTGCCCCAGCAAG 240  
Qy 241 GCGAGGACACCTCTGAGGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 300  
Db 241 GCGAGGACACCTCTGAGGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 300  
Qy 301 CTGCTAGGCCCAACCGCCACCCAGAGTCTCTAGGGCCAGTGAAGATGGACCCCTCAACA 360  
Db 301 CTGCTAGGCCCAACCGCCACCCAGAGTCTCTAGGGCCAGTGAAGATGGACCCCTCAACA 360  
Qy 361 GCAGGGCCATCTCCCTCGAGATATGAGTTGGACAGAGACTTGNACCGGCTCCCCCAGG 420  
Db 361 GCAGGGCCATCTCCCTCGAGATATGAGTTGGACAGAGACTTGNACCGGCTCCCCCAGG 420  
Qy 421 ACCTGTACCGCCGCTGTGCTGTGCCCGCACTGGCTCAGCTACAGACAGGCTCCCAACA 480  
Db 421 ACCTGTACCGCCGCTGTGCTGTGCCCGCACTGGCTCAGCTACAGACAGGCTCCCAACA 480  
Qy 481 TGGACCCCGGGGCAACTCGGAGTGTCTTACCAACAACAGACTGTCTTACCGGGCGC 540  
Db 481 TGGACCCCGGGGCAACTCGGAGTGTCTTACCAACAACAGACTGTCTTACCGGGCGC 540  
Qy 541 CATGCCATGGCGAGAGGCAACCCACAGGCTACTGCTGAGCGGAGGCTGTACCCGTG 600  
Db 541 CATGCCATGGCGAGAGGCAACCCACAGGCTACTGCTGAGCGGAGGCTGTACCCGTG 600  
Qy 601 TTTCCTTAGCTTGTGTGTGTGGGCGCCCGTGTGATGGGCTAG 644  
Db 601 TTTCCTTAGCTTGTGTGTGTGGGCGCCCGTGTGATGGGCTAG 644











Db	939	GCTTACCGAGTCCTTGCTGGCTTGTTGTGTGTCGGCCGCCGGGTCAATGGCTTAG	993
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LOCUS	Sequence 3 from Patent WO01/9288.	985 bp	DNA linear PAT 26-NOV-2001
DEFINITION	AX299775		
ACCESSION	AX299775		
VERSION	AX299775.1	GI:17129296	
KEYWORDS	unidentified.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1		
AUTHORS	Hurst, S.D., Zurawski, S.M. and Rennick, D.M.		
TITLE	Cytokine uses; compositions; methods		
JOURNAL	Patent: WO 01/9288-A 3 25-OCT-2001;		
FEATURES	SCHERING CORPORATION (US)		
source	Location/Qualifiers		
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	/note="murine IL-174 polynucleotide sequence"		
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	/note="unnamed protein product"		
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	/protein_id="CADL2719.1"		
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	/translation="MTQAVAFAMIVGTHTVLSRIQEGCSHLPSGPCSKQEPEPMELKMSASVSPPPEPUSHHTHAECRASDKDPLNSRAISPSYELDRLNRPVDLYHARC		
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	/product="unnamed"		
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	Best Local Similarity	81.0%; Pred. No. 1.9e-72;	
	Matches	413; Conservative 0; Mismatches 73; Indels 24; Gaps 1;	
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DB	1	ATGTACCAGGCTGTTGCATTCTTTGGCAATGATCTGGGAACCCACACCTCACAGTTCGGG	60
QY	213	-----CACTGGCCCCAGCTGCTGCTCCCAGCAAAGGGGAGGACACCTCT	254
DB	61	ATCCAGGAGSGCTGCAGTCACTTGCCTGCTGCTCCCAGCAAAGAACCAACCCCG	120
QY	255	GAGGAGCTGTGAGGTGGAGCACTGTCCTGCTGCTCCCAGCAAGCATGTAGCGCCCAAC	314
DB	121	GAGGAGTGGCTGAAGTGGAGCTCTGCATCTGTGTCCTCCCAGAGCCTCTGTAGCCACAC	180
QY	315	CGCCACCCAGACTCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCTCC	374
DB	181	CACACGCAGAATCTCTGACGGGCCAGCAAGATGGGCCCTCAACAGCAGGGCCATCTCT	240
QY	375	CCCTGGAGATATGATTGGACAGACTTGAACCGGCTCCCCAGGACCTGTACCAGCC	434
DB	241	CCTGGAGCTATGAGTTGGACAGGACTTGAATCGGGTCCCCAGGACCTGTACCAGCT	300
QY	435	CGTTGGCTGTGCCCGCACTCGCTCAGCCTACAGACAGGCTCCACATGGACCCCGGGC	494
DB	301	CGATGCTGTGCCCACTCGCTCAGCCTACAGAGGCTCCACATGGACCCCGTGGGC	360
QY	495	AACTCGAGCTGCTCTACCAACACACAGACTGTCTTACCGGGCGGCGAATGCCATGGCGAG	554
DB	361	AACTCGGTCCCACTTTACCACAACACAGACGGTCTTCTACCGGGGGCCATGCCATGTGAG	420
QY	555	AAGGGACCCCAACAGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTACGCTTGT	614
DB	421	GAAGGTACCCATCGCCGCTACTCTTTGGAGCGCAGGCTCTACCGAGCTCTCTTGGCTTGT	480



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Overall quality chart :
Range : bases
0 - 26
1 - 9
10 - 19
20 - 29
30 - 39
40 - 49
50 - 59
60 - 69
70 - 79
80 - 89
90 - 99

Percentage of bases with a quality value >= 40 : 99 %
Location/Qualifiers
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/chromosome="14"
/clone_lib="Caltech-D"
/clone="C-2201G16"
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RHdb:RH92419
dbSTS:STS63422
Identified using the e-PCR software (G. Schuler)"
/note="matching EMBL:N91549
RHdb:RH76320
dbSTS:STS53407
Identified using the e-PCR software (G. Schuler)"
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/note="matching EMBL:X52889
RHdb:RH96140
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39479 a 37198 c 39593 g 41638 t 2 others

BASE COUNT 39479 a 37198 c 39593 g 41638 t 2 others

Query Match 39.8% Score 256; DB 9; Length 157910;
Best Local Similarity 100.0%; Pred. No. 8.7e-53;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 389 GTTGACAGAGACTTGACCGCTCCCGGAGACCTGTACACGCGCCGTGCTGTGCGCC 448
Db 9616 GTTGACAGAGACTTGACCGCTCCCGGAGACCTGTACACGCGCCGTGCTGTGCGCC 9675

Oy 449 GCACTGCTCAGCTTACAGAGAGTCCACATGGACCCCGGCGCACTCGAGCTGCT 508
Db 9676 GCACTGCTCAGCTTACAGAGAGTCCACATGGACCCCGGCGCACTCGAGCTGCT 9735

Oy 509 CTACACACAGAGTCTTCTACCGGCGCATGCCATGCCATGCCAGGACCCACCA 568
Db 9736 CTACACACAGAGTCTTCTACCGGCGCATGCCATGCCATGCCAGGACCCACCA 9795

Oy 569 GGGCTACTGCTGAGCGGAGCTGTACCGTCTTCTTCTAGTGTGTGTGTGCGGCC 628
Db 9796 GGGCTACTGCTGAGCGGAGCTGTACCGTCTTCTTCTAGTGTGTGTGTGCGGCC 9855

Oy 629 CGGTGTGATGGGCTAG 644
Db 9856 CGGTGTGATGGGCTAG 9871

RESULT 15
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LOCUS Human chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11
DEFINITION Human chromosome 14 of Homo sapiens (Human), complete sequence.
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ACCESSION AL049829
VERSION AL049829.4 GI:8217859
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 196292)
Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,
Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C.,
Gyapay, G., Saurin, W. and Weissensbach, J.
Sequencing of the human chromosome 14
Unpublished
2 (bases 1 to 196292)
Genoscope.
Direct Submission
Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Jun 3, 2000 this sequence version replaced gi:6138746.
-----
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
-----
The following BAC sequence is oriented from the 17 to the SP6 end.
Upstream BAC (overlapping the 17 end) : R-244E17
Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC=AL132855)
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Assembly program: Phrap; version 2.0
Quality coverage: 7.94x in Q20 bases; sum-of-contigs
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Overall quality chart :
Range : bases
0 - 9
10 - 19
20 - 29
30 - 39
40 - 49
50 - 59
60 - 69
70 - 79
80 - 89
90 - 99

Percentage of bases with a quality value >= 40 : 99 %
Location/Qualifiers
1. 196292
/organism="Homo sapiens"
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/chromosome="14"
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dbSTS:STS69699
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Best Local Similarity 100.0%; Pred. No. 8.8e-53;  
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QY 449 GCACCTGGCTACAGAGGCTCCACATGACCGCCCGGGGCAACTCGGAGCTGCT 508  
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Db 157743 GCACCTGGCTACAGAGGCTCCACATGACCGCCCGGGGCAACTCGGAGCTGCT 157802  
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QY 569 GGGCTACTGCTGAGCGGCGGCTGTACCGGTTTCCCTTAGCTTGTGTGTGCGGCC 628  
|||||  
Db 157863 GGGCTACTGCTGAGCGGCGGCTGTACCGGTTTCCCTTAGCTTGTGTGTGCGGCC 157922  
QY 629 CCGTGTGATGGGCTAG 644  
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Db 157923 CCGTGTGATGGGCTAG 157938

Search completed: May 12, 2003, 01:39:15  
Job time : 1650 secs



Matches	77;	Conservative	0;	Mismatches	70;	Indels	0;	Gaps	0;
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DB	585	TGAAGGAGACACCATCTGACACGATGGACGTTGAGGTGCTGGAGCTCTGCACCAAGAC	526						
QY	206	CTACAGCCACTGGCCCGCAGCTGCTGCCCCAGCAAAAGGCGAGGACCACTCTGAGGAGCTGCT	265						
DB	525	GGTCACCAGCACCCCGCATCACCAGCCCCCAACAAAGGTTGGACATAATAGAGCTGTTGCT	466						
QY	266	GAGGTGGAGCACTGTGCCTGTGCCTCC	292						
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US-09-553-132-1/c									
; Sequence 1, Application US/09553132									
; Patent No. 6350858									
; GENERAL INFORMATION:									
; APPLICANT: FEILD, JOHN									
; TITLE OF INVENTION: A HUMAN SODIUM DEPENDENT PHOSPHATE									
; TITLE OF INVENTION: TRANSPORTER (IPT-1)									
; FILE REFERENCE: GH-70006-D1									
; CURRENT APPLICATION NUMBER: US/09/553,132									
; CURRENT FILING DATE: 2000-04-19									
; PRIOR APPLICATION NUMBER: 60/044,974									
; PRIOR FILING DATE: 1997-04-28									
; PRIOR APPLICATION NUMBER: 08/935,433									
; PRIOR FILING DATE: 1997-09-23									
; NUMBER OF SEQ ID NOS: 4									
; SOFTWARE: FastSeq for Windows Version 3.0									
; SEQ ID NO 1									
; LENGTH: 2288									
; TYPE: DNA									
; ORGANISM: HOMO SAPIENS									
US-09-553-132-1									
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Best Local Similarity 52.4%; Pred. No. 2.6;									
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DB	585	TGAAGGAGACACCATCTGACACGATGGACGTTGAGGTGCTGGAGCTCTGCACCAAGAC	526						
QY	206	CTACAGCCACTGGCCCGCAGCTGCTGCCCCAGCAAAAGGCGAGGACCACTCTGAGGAGCTGCT	265						
DB	525	GGTCACCAGCACCCCGCATCACCAGCCCCCAACAAAGGTTGGACATAATAGAGCTGTTGCT	466						
QY	266	GAGGTGGAGCACTGTGCCTGTGCCTCC	292						
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US-09-499-964-2/c									
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; Patent No. 6380374									





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Db 1353 GGGGCTGATGAAGAGCAGTACGAGGCGAGGCTGTGCTGTCAACGAGCGCGGCAACG 1412  
QY 445 GCGCGCAGTGGCTACGCTACAGACAGGCTCCACATGACACCCCGGGGCAACTCGGAGC 504  
Db 1413 GCACCTACACCGTCACTCAACAGCTCACCAGTACAGGCGCGGCTTCTACTGGTGG 1472  
QY 505 TGCTCTACCAAC 518  
Db 1473 TGACCGAGCGGAC 1486

## RESULT 7

US-09-312-157-5  
; Sequence 5, Application US/09312157  
; Patent No. 6303341  
; GENERAL INFORMATION:  
; APPLICANT: ANDREW C. HIATT, JULIAN  
; K.-C. MA, THOMAS LEHNER  
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION  
; PROTEINS IN PLANTS AND THEIR USES

NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESS: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/312,157

FILING DATE: 14-May-1999

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/434,000

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.

REGISTRATION NUMBER: 34,613

REFERENCE/DOCKET NUMBER: 212/127

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 552-8400

TELEFAX: (619) 552-0159

TELEX: 67-351

SEQUENCE LISTING

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 3630 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

DESCRIPTION: Bovine Polymunoglobulin Receptor

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 152.....2425

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-312-157-5

Query Match 5.4%; Score 34.8; DB 4; Length 3630;  
Best Local Similarity 46.1%; Pred. No. 3.5;  
Matches 117; Conservative 0; Mismatches 137; Indels 0; Gaps 0;  
QY 265 TGAGTTGGACACTGTGCTGTGCTCCCTTAGAGCCTGTAGCCCAACCCGACCCAG 324  
Db 1233 TGAGGGAGGCTCTGTGACTGTATCTTGCCCTTACAACTTAAGGATGCCAACAGGCGCA 1292  
QY 325 AGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCTCCCCCTGGAGAT 384  
Db 1293 AGTACTGGTGTCACTGGGAAGAGGCTCAAAACGGCCGCTGCCCGGCTGGTGGAGAGCC 1352  
QY 385 ATGAGTTGACAGAGACTTGAACCGGCTCCCCAGGACCTGTACCAACGCGCCGTTGGCTGT 444  
Db 1353 GGGGCTGTGATGAAGAGCAGTACGAGGCGAGGCTGTGCTGTCAACGAGCGCGGCAACG 1412  
QY 445 GCGCGCAGTGGCTACGCTACAGACAGGCTCCACATGACACCCCGGGGCAACTCGGAGC 504  
Db 1413 GCACCTACACCGTCACTCAACAGCTCACCAGTACAGGCGCGGCTTCTACTGGTGG 1472  
QY 505 TGCTCTACCAAC 518  
Db 1473 TGACCGAGCGGAC 1486

## RESULT 8

US-09-287-354-1/c  
; Sequence 1, Application US/09287354  
; Patent No. 6348348

GENERAL INFORMATION:

APPLICANT: THOMPSON, Catherine C.

TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN

FILE REFERENCE: Thompson-20263/0243435

CURRENT APPLICATION NUMBER: US/09/287,354

CURRENT FILING DATE: 1999-04-07

EARLIER APPLICATION NUMBER: US 60/080,888

EARLIER FILING DATE: 1998-04-07

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 3202

TYPE: DNA

ORGANISM: Homo sapiens

US-09-287-354-1

Query Match 5.4%; Score 34.6; DB 4; Length 3202;

Best Local Similarity 46.8%; Pred. No. 3.8;

Matches 109; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 354 CTCACAGCAGGGCCATCTCCCTCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTC 413

Db 2838 CTGAGCAGAGAGGGCAGAGGCTCTCAGGGGAGGAGAAAGTGTGAGTGTGAGTGTGCT 2779

QY 414 CCCAGGACCTGTACACGCGCTTGTGCTGTCGCCGCACTGCTGCTGCTGCTGCTGCTGCT 473

Db 2778 CACACGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2719

QY 474 TCCACATGGACCCCGGGGCAACTCGGAGTGTCTTCTACCAACAGAGACTGTCTTCTAC 533

Db 2718 CTGGAGCAGGGTCCAGCAGCTCAGCCCTCTCTCCCGAGGGCGCCGCGGAGGCTGCT 2659

QY 534 CGCGGCGCATGCCATGGCGAGAGGGCACCCACAAAGGGCTACTGCTGGAGCG 586

Db 2658 ATCCAGGTAGCAGCTGCTGCGGGGCGCCAGGCTCCAGGGCGGCTGCCCGGCGG 2606

## RESULT 9

US-08-148-910-14

; Sequence 14, Application US/08148910

; Patent No. 5466593

GENERAL INFORMATION:

APPLICANT: Takeshi SHIMOMURA et al.

TITLE OF INVENTION: NO. 5466593e1 Protein and Gene Encoding Said Protein









GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 01:08:34 ; Search time 93 Seconds  
(without alignments)  
8605.398 Million cell updates/sec

Title: US-10-037-591A-1

Perfect score: 644

Sequence: 1 ctcaagtcactccctcaaaaa.....ggcccggtgatggcgtag 644

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Gapop 10.0 , Gapext 1.0

Searched: 783854 seqs, 621352466 residues

Total number of hits satisfying chosen parameters: 1567708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications\_NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
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- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	644	100.0	644	10	US-09-886-404-1
2	478.4	74.3	1320	9	US-09-874-503-5
3	478.4	74.3	1320	9	US-10-000-157-5
4	478.4	74.3	1320	9	US-10-063-547-155
5	478.4	74.3	1320	9	US-09-747-259-5
6	478.4	74.3	1320	9	US-10-063-616-155
7	478.4	74.3	1320	9	US-10-063-502-155
8	478.4	74.3	1320	9	US-10-063-518-155
9	478.4	74.3	1320	9	US-10-063-598-155
10	478.4	74.3	1320	9	US-10-227-693-155
11	478.4	74.3	1320	9	US-09-908-827-5
12	478.4	74.3	1320	9	US-10-213-181-17
13	478.4	74.3	1320	9	US-10-063-567-155
14	478.4	74.3	1320	9	US-10-063-599-155
15	478.4	74.3	1320	9	US-10-212-912-17
16	478.4	74.3	1320	9	US-10-213-044-17
17	478.4	74.3	1320	9	US-10-063-595-155
18	478.4	74.3	1320	12	US-10-006-867-155
19	336.8	52.3	1013	10	US-09-886-404-3

20	336.2	52.2	1496	10	US-09-886-404-9	Sequence 9, Appli
21	55.4	8.6	1067	9	US-09-320-713-28	Sequence 28, Appl
22	55.4	8.6	1067	10	US-09-731-816-28	Sequence 28, Appl
23	53.8	8.4	594	10	US-09-854-280-17	Sequence 17, Appl
24	53.8	8.4	594	10	US-09-854-208-17	Sequence 17, Appl
25	53.8	8.4	1047	9	US-09-874-503-3	Sequence 3, Appli
26	53.8	8.4	1047	9	US-10-000-157-3	Sequence 3, Appli
27	53.8	8.4	1047	9	US-10-036-041-10	Sequence 10, Appl
28	53.8	8.4	1047	9	US-09-747-259-3	Sequence 3, Appli
29	53.8	8.4	1047	9	US-10-035-855-10	Sequence 10, Appl
30	53.8	8.4	1047	9	US-10-174-590-47	Sequence 447, App
31	53.8	8.4	1047	9	US-10-176-758-447	Sequence 447, App
32	53.8	8.4	1047	9	US-10-175-737-447	Sequence 447, App
33	53.8	8.4	1047	9	US-10-173-706-447	Sequence 447, App
34	53.8	8.4	1047	9	US-10-175-738-447	Sequence 447, App
35	53.8	8.4	1047	9	US-10-175-752-447	Sequence 447, App
36	53.8	8.4	1047	9	US-10-176-482-447	Sequence 447, App
37	53.8	8.4	1047	9	US-10-176-757-447	Sequence 447, App
38	53.8	8.4	1047	9	US-10-176-913-447	Sequence 447, App
39	53.8	8.4	1047	9	US-10-180-552-447	Sequence 447, App
40	53.8	8.4	1047	9	US-10-180-557-447	Sequence 447, App
41	53.8	8.4	1047	9	US-09-931-836-10	Sequence 10, Appl
42	53.8	8.4	1047	9	US-10-173-700-447	Sequence 447, App
43	53.8	8.4	1047	9	US-10-174-572-447	Sequence 447, App
44	53.8	8.4	1047	9	US-10-174-579-447	Sequence 447, App
45	53.8	8.4	1047	9	US-10-174-582-447	Sequence 447, App

#### ALIGNMENTS

##### RESULT 1

US-09-886-404-1  
; Sequence 1, Application US/09886404  
; Patent No. US20020037524A1  
; GENERAL INFORMATION:  
; APPLICANT: Medlock, Eugene  
; APPLICANT: Yeh, Richard  
; APPLICANT: Silbiger, Scott M.  
; APPLICANT: Elliot, Gary S.  
; APPLICANT: Nguyen, Hung Q.  
; APPLICANT: Jing, Shuguan  
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof  
; FILE REFERENCE: 01017/37128B  
; CURRENT APPLICATION NUMBER: US/09/886,404  
; CURRENT FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 09/810,384  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/266,159  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/213,125  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 644  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (159)...(641)  
US-09-886-404-1

Query Match 100.0%; Score 644; DB 10; Length 644;  
Best Local Similarity 100.0%; Pred. No. 2.2e-196;  
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAAGTCACCTCCCTAAAAAGACAGTGAATAAATTTGAATAAACAACAGGTTGCT 60  
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Db 1 CTCAAGTCACCTCCCTAAAAAGACAGTGAATAAATTTGAATAAACAACAGGTTGCT 60  
|||||

QY 61 GAAATAAATTCAGACTCTTAACCTGCTCAGTCAGCCTGCTCCAGAGGCTGTAC 120  
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Db 61 GAAATATAAATCAGGACTCCTAACCTGCTCCAGCTGCTTCCACGAGGCTCTCAG 120  
QY 121 TCAGTCCCCACTTGTGACTGAGTGTGAGTGCAGTGCCAGCAGTGTACCAAGGTGGTTCATTCT 180  
Db 121 TCAGTCCCCACTTGTGACTGAGTGTGAGTGCAGTGCCAGCAGTGTACCAAGGTGGTTCATTCT 180  
QY 181 TGGCAATGTCATGGAAGCCACACCTACAGCCACTTGGCCAGCTGCTGCCGCCAGCAAG 240  
Db 181 TGGCAATGTCATGGAAGCCACACCTACAGCCACTTGGCCAGCTGCTGCCGCCAGCAAG 240  
QY 241 GGCAGACACCTCTGAGGAGCTGCTGAGGTGGAGCAGTGTGCTGTGCTCCCTAGAGC 300  
Db 241 GGCAGACACCTCTGAGGAGCTGCTGAGGTGGAGCAGTGTGCTGTGCTCCCTAGAGC 300  
QY 301 CTGCTAGGCCCAACCCGCCACCCAGAGTCTCTGTAGGGCCAGTGAAGATGGACCCCTCAACA 360  
Db 301 CTGCTAGGCCCAACCCGCCACCCAGAGTCTCTGTAGGGCCAGTGAAGATGGACCCCTCAACA 360  
QY 361 GCAGGCCCATCTCCCTCTGGAGATATGAGTTGGACAGAGACTTGAACCCGCTCCCCCAGG 420  
Db 361 GCAGGCCCATCTCCCTCTGGAGATATGAGTTGGACAGAGACTTGAACCCGCTCCCCCAGG 420  
QY 421 ACCTGTACCAGCCCGCTGCTGCTGCCCGCAGTGCCTGAGCCCTACAGACAGGCTCCCA 480  
Db 421 ACCTGTACCAGCCCGCTGCTGCTGCCCGCAGTGCCTGAGCCCTACAGACAGGCTCCCA 480  
QY 481 TGGACCCCGGGGCAACTCGAGCTGCTTACCAACACCAAGAGTGTCTTACCGGGCGG 540  
Db 481 TGGACCCCGGGGCAACTCGAGCTGCTTACCAACACCAAGAGTGTCTTACCGGGCGG 540  
QY 541 CATGCCATGGCGAAGAGGGGCCACCAAGGGCTACTGCCCTGGAGCGGAGCTGTACCGTG 600  
Db 541 CATGCCATGGCGAAGAGGGGCCACCAAGGGCTACTGCCCTGGAGCGGAGCTGTACCGTG 600  
QY 601 TTTCCTTAGCTTGTGTGTGTGTCGGCGCCGCTGTGTGCTAG 644  
Db 601 TTTCCTTAGCTTGTGTGTGTGTCGGCGCCGCTGTGTGCTAG 644

RESULT 2

US-09-874-503-5

Sequence 5, Application US/09874503

Patent No. US2002017718A1

GENERAL INFORMATION:

APPLICANT: Chen, Jian

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Li, Hanzhong

APPLICANT: Hillan, Kenneth J.

APPLICANT: Hymowitz, Sarah G.

APPLICANT: Tumas, Daniel

APPLICANT: Starovasnik, Melissa A.

APPLICANT: VanLookeren, Menno

APPLICANT: Vandlen, Richard

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Yansura, Daniel

TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

FILE REFERENCE: P1361R1P3(US)

CURRENT APPLICATION NUMBER: US/09/874,503

CURRENT FILING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: US 60/253,646

PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: US 60/244,072

PRIOR FILING DATE: 2000-10-26

PRIOR APPLICATION NUMBER: US 60/242,837

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/175,481

PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: US 60/191,007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/213,807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 60/172,096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: US 60/138,387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: US 60/134,287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US 60/131,022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: US 60/130,232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: US 60/113,621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 60/085,579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: US 09/854,208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/854,280  
PRIOR FILING DATE: 2001-05-20  
PRIOR APPLICATION NUMBER: US 09/816,744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: US 09/747,259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US 09/644,848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: US 09/380,142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: US 09/380,138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: US 09/311,832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: US PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: US PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: US PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US PCT/US00/05601  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: US PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: US PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 5  
LENGTH: 1320  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-09-874-503-5

Query Match 74.3%; Score 478.4; DB 9; Length 1320;  
Best Local Similarity 99.8%; Pred. No. 3.9e-143;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 165 CAGGTGTTGCAATCTTTGGCAATGCTATGGGAACCCACACCTACAGCCACTGGCCACG 224



Db 313 CAGGTGGTTCATTCTTGGCAATGGTCTATGGAAACCCACACCTACAGCCACTGCCCCAGC 372  
QY 225 TGCTGCCCGCAGAAAGGCGAGGACACCTCTGAGAGAGTGTGAGGTGGAGCACTGTGCCT 284  
Db 373 TGCTGCCCGCAGAAAGGCGAGGACACCTCTGAGAGAGTGTGAGGTGGAGCACTGTGCCT 432  
QY 285 GTGCCTCCCTTAGAGCTGTAGGCCCAACCGCCACCCAGAGTCTGTAGGGCCAGTGAA 344  
Db 433 GTGCCTCCCTTAGAGCTGTAGGCCCAACCGCCACCCAGAGTCTGTAGGGCCAGTGAA 492  
QY 345 GATGGACCCCTCAACACGAGGGCCATCTCCCTCTGGAGATATGATTTGGACAGAGACTTG 404  
Db 493 GATGGACCCCTCAACACGAGGGCCATCTCCCTCTGGAGATATGATTTGGACAGAGACTTG 552  
QY 405 AACCGGCTCCCGCAGGACCTGTACCCAGCGCCGTTGCTGTGCCGCACTGGGTGAGCCTA 464  
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QY 465 CACAGAGGCTCCACATGAGACCCCGGGGCAACTCGGAGCTGTCTACCAACACGAGACT 524  
Db 613 CACAGAGGCTCCACATGAGACCCCGGGGCAACTCGGAGCTGTCTACCAACACGAGACT 672  
QY 525 GTCTTCTACGGCGGCCATGCCATGGCGAGAAGGCGCACCAAGGGCTACTGCTCTGGAG 584  
Db 673 GTCTTCTACGGCGGCCATGCCATGGCGAGAAGGCGCACCAAGGGCTACTGCTCTGGAG 732  
QY 585 CGAGGCTGTACCGTGTCTTCTAGCTGTGTGTGTGGGCCCCCTGTGATGGGCTAG 644  
Db 733 CGAGGCTGTACCGTGTCTTCTAGCTGTGTGTGTGGGCCCCCTGTGATGGGCTAG 792

RESULT 3

US-10-000-157-5  
; Sequence 5, Application US/10000157  
; Publication No. US20020182673A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jian  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul L.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Hymowitz, Sarah  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Starovasinik, Melissa.  
; APPLICANT: VanLookeren, Menno  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William  
; APPLICANT: Yansura, Daniel  
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
; FILE REFERENCE: P1381R1P4(US)  
; CURRENT APPLICATION NUMBER: US/10/000,157  
; CURRENT FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/113621  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/130232  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: 60/131022  
; PRIOR FILING DATE: 1999-04-26  
; PRIOR APPLICATION NUMBER: 60/134287  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 60/138387  
; PRIOR FILING DATE: 1999-06-09  
; PRIOR APPLICATION NUMBER: 60/172096  
; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 60/175481  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 60/191007  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/213807  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: 60/242837  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 60/244072  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: 60/253646  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 09/311832  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 09/380138  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: 09/380142  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: 09/644848  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 09/747259  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 09/816744  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 09/854208  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/854280  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/874503  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: 09/908827  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 09/929404  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: 09/931836  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: PCT/US99/05028  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: PCT/US99/10733  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: PCT/US99/31274  
; PRIOR FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: PCT/US00/04341  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/US00/05601  
; PRIOR FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: PCT/US00/07532  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: PCT/US00/23328  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: PCT/US00/30873  
; PRIOR FILING DATE: 2000-11-10  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US00/34956  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: PCT/US01/17800  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: PCT/US01/19692  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: PCT/US01/21066  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: PCT/US01/21735  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 39









1	PRIOR FILING DATE: 2000-10-24,	
2	PRIOR APPLICATION NUMBER: 60/244,072	
3	PRIOR FILING DATE: 2000-10-26,	
4	PRIOR APPLICATION NUMBER: 2000-10-26	
5	PRIOR FILING DATE: 1999-05-14	
6	PRIOR APPLICATION NUMBER: 09/311,832	
7	PRIOR FILING DATE: 1999-05-14	
8	PRIOR APPLICATION NUMBER: 09/380,138	
9	PRIOR FILING DATE: 1999-08-25	
10	PRIOR APPLICATION NUMBER: 09/380,142	
11	PRIOR FILING DATE: 1999-08-25	
12	PRIOR APPLICATION NUMBER: 09/644,848	
13	PRIOR FILING DATE: 2000-08-22	
14	PRIOR APPLICATION NUMBER: 09/747,259	
15	PRIOR FILING DATE: 2000-12-20	
16	PRIOR APPLICATION NUMBER: 09/816,744	
17	PRIOR FILING DATE: 2001-03-22	
18	PRIOR APPLICATION NUMBER: 09/854,208	
19	PRIOR FILING DATE: 2001-05-10	
20	PRIOR APPLICATION NUMBER: 09/854,280	
21	PRIOR FILING DATE: 2001-05-10	
22	PRIOR APPLICATION NUMBER: PCT/US99/05028	
23	PRIOR FILING DATE: 1999-03-08	
24	PRIOR APPLICATION NUMBER: PCT/US99/10733	
25	PRIOR FILING DATE: 1999-05-14	
26	PRIOR APPLICATION NUMBER: PCT/US99/31274	
27	PRIOR FILING DATE: 1999-12-30	
28	PRIOR APPLICATION NUMBER: PCT/US00/04341	
29	PRIOR FILING DATE: 2000-02-18	
30	PRIOR APPLICATION NUMBER: PCT/US00/05601	
31	PRIOR FILING DATE: 2000-03-01	
32	PRIOR APPLICATION NUMBER: PCT/US00/05841	
33	PRIOR FILING DATE: 2000-03-02	
34	PRIOR APPLICATION NUMBER: PCT/US00/07532	
35	PRIOR FILING DATE: 2000-03-21	
36	PRIOR APPLICATION NUMBER: PCT/US00/15364	
37	PRIOR FILING DATE: 2000-06-02	
38	PRIOR APPLICATION NUMBER: PCT/US00/23328	
39	PRIOR FILING DATE: 2000-08-24	
40	PRIOR APPLICATION NUMBER: PCT/US00/30873	
41	PRIOR FILING DATE: 2000-11-10	
42	PRIOR APPLICATION NUMBER: PCT/US00/32678	
43	PRIOR FILING DATE: 2000-12-01	
44	PRIOR APPLICATION NUMBER: PCT/US00/34956	
45	PRIOR FILING DATE: 2000-12-20	
46	PRIOR APPLICATION NUMBER: PCT/US01/06520	
47	PRIOR FILING DATE: 2001-02-28	
48	NUMBER OF SEQ ID NOS: 39	
49	SEQ ID NO 5	
50	LENGTH: 1320	
51	TYPE: DNA	
52	ORGANISM: Homo Sapien	
53	US-908-827-5	

	Query Match	74.3%;	Score 478.4;	DB 9;	Length 1320;
	Best Local Similarity	99.8%;	Pred. No. 3.9e-143;		
	Matches 479; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	165	CAGTGGTTGCATCTTTGGCAATGTCATGGAAACCCACACTCAGCGCACTTGCCACAGC	224		
Db	313	CAGTGGTTGCATCTTTGGCAATGTCATGGAAACCCACACTCAGCGCACTTGCCACAGC	372		
QY	225	TGCTGCCCCACAAGGCGAGCACCTCTCAGGAGCTGTGAGTGAGGACACTGTGGCT	284		
Db	373	TGCTGCCCCACAAGGCGAGCACCTCTCAGGAGCTGTGAGTGAGGACACTGTGGCT	432		
QY	285	GTGCCTTCCCCTTAGAGCCTGCTTAGGCCAACCCGACCAGAGTCTCTTAGGCCCAAGTGA	344		
Db	433	GTGCCTTCCCCTTAGAGCCTGCTTAGGCCAACCCGACCAGAGTCTCTTAGGCCCAAGTGA	492		
QY	345	GATGGACCCCTCAACAGCAGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTG	404		
Db	493	GATGGACCCCTCAACAGCAGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTG	552		
QY	405	AACCGGGTCCCCCAGGACCTGTACACAGCCCGTTGCTGTGCGCCGCACTGGGTACGCCTA	464		

Db	553	AACCGGGTCCCGCCAGAGCTGTACACAGCCCGTGGCTGTGCCCCGACTGGGTACGCCCTA	612
Qy	465	CAGACAGGCTCCACACATGGACACCCCGGGGCAACTCGGAGCTGCTTACCACAACACAGACT	524
Db	613	CAGACAGGCTCCACACATGGACACCCCGGGGCAACTCGGAGCTGCTTACCACAACACAGACT	672
Qy	525	GTCTTTCACGGGGGGCCATGCCATGCCGAGAGAGGGACCCACAAAGGGCTACTGCCCTGGAG	584
Db	673	GTCTTTCACAGGGGGGCATGCCATGCCGAGAGAGGGACCCACAAAGGGCTACTGCCCTGGAG	732
Qy	585	CGCAGGCTGACCGTGTCTTCCCTTAGCTTGTGTGTGTCGGCCCGCTGTGATGGGCTAG	644
Db	733	CGCAGGCTGACCGTGTCTTCCCTTAGCTTGTGTGTGTCGGCCCGCTGTGATGGGCTAG	792

RESULT 12

US-10-213-181-17

; Sequence 17, Application US/10213181

; Publication No. US20030054484A1

; GENERAL INFORMATION:

; APPLICANT: Fong, Sherman

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin

; APPLICANT: Wood, William

; APPLICANT: Zhang, Wemin

; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune

; TITLE OF INVENTION: Related Diseases

; FILE REFERENCE: P3133RIC7

; CURRENT APPLICATION NUMBER: US/10/213,181

; CURRENT FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: US 10/052,594

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: PCT/US00/30873

; PRIOR FILING DATE: 2000-11-10

; PRIOR APPLICATION NUMBER: US 60/177,118

; PRIOR FILING DATE: 2000-01-20

; NUMBER OF SEQ ID NOS: 24

; SEQ ID NO 17

; LENGTH: 1320

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-213-181-17

	Query Match	74.3%;	Score 478.4;	DB 9;	Length 1320;
	Best Local Similarity	99.8%;	Pred. No. 3.9e-143;		
	Matches 479;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps
Qy	165	CAGGTGTTGCATCTTGGCAATGTCATGGGAACCCACACCTACAGCCACTTGSCCCAGC	224		
Db	313	CAGGTGTTGCATCTTGGCAATGTCATGGGAACCCACACCTACAGCCACTTGSCCCAGC	372		
Qy	225	TGCTGCCCCAGCAAAGGCGAGGACACCTCTGAGGAGCTCTGAGGTGGAGCACTGTGCCT	284		
Db	373	TGCTGCCCCAGCAAAGGCGAGGACACCTCTGAGGAGCTCTGAGGTGGAGCACTGTGCCT	432		
Qy	285	GTGCCTCCCCTAGAGCTGCTAGGCGCCAAACGCCACCCAGAGTCTGTAGGCGCCAGTAA	344		
Db	433	GTGCCTCCCCTAGAGCTGCTAGGCGCCAAACGCCACCCAGAGTCTGTAGGCGCCAGTAA	492		
Qy	345	GATGGACCCCTCAACAGCAGGGGCCATCTCCCCTGGAGATATAGATTGGACAGAGACTTG	404		
Db	493	GATGGACCCCTCAACAGCAGGGGCCATCTCCCCTGGAGATATAGATTGGACAGAGACTTG	552		
Qy	405	AACGGGTGCCCCAGGACCTGTATACCAGGCCCGTTGGCTCTGGCCCGCACTGCCTCAGCCCTA	464		
Db	553	AACGGGTGCCCCAGGACCTGTATACCAGGCCCGTTGGCTCTGGCCCGCACTGCCTCAGCCCTA	612		

[illegible]



Mon May 12 08:06:50 2003

```

; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P3133RIC2
; CURRENT APPLICATION NUMBER: US/10/212,912
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/052,594
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/172,059
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 17
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-212-912-17

Query Match      74.3%; Score 478.4; DB 9; Length 1320;
Best Local Similarity 99.8%; Pred. No. 3.9e-143;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 165 CAGGTGGTTCATCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGCCCCAGC 224
DB 313 CAGGTGGTTCATCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGCCCCAGC 372

QY 225 TGCCTGCCACAGAAAGGCGAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 284
DB 373 TGCCTGCCACAGAAAGGCGAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 432

QY 285 GTGCCTCCCTTAGAGCTGCTAGGCCCAACCGCCACCCAGAGTCCCTGTAGGGCCAGTGAA 344
DB 433 GTGCCTCCCTTAGAGCTGCTAGGCCCAACCGCCACCCAGAGTCCCTGTAGGGCCAGTGAA 492

QY 345 GATGGACCCCTCAACAGCAGGCGCATCTCCCTGGAGATATGAGTTGGACAGAGACTTG 404
DB 493 GATGGACCCCTCAACAGCAGGCGCATCTCCCTGGAGATATGAGTTGGACAGAGACTTG 552

QY 405 AACCGGCTCCCGCAGGACCTGTACACGCGCCGTTGCTGTGCCGCACTGCGTCAGCCTA 464
DB 553 AACCGGCTCCCGCAGGACCTGTACACGCGCCGTTGCTGTGCCGCACTGCGTCAGCCTA 612

QY 465 CAGACAGGCTCCACATGAGACCCCGGGGGCAACTCGGAGCTGCTTACCAACACCACT 524
DB 613 CAGACAGGCTCCACATGAGACCCCGGGGGCAACTCGGAGCTGCTTACCAACACCACT 672

QY 525 GTCTTACCGCGGCGCATGCCATGGGAGAGGACCCACACAGGCGCTACTGCTGGAG 584
DB 673 GTCTTACCGCGGCGCATGCCATGGGAGAGGACCCACACAGGCGCTACTGCTGGAG 732

QY 585 CGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGGGGCCCGCTGTGATGGGCTAG 644
DB 733 CGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGGGGCCCGCTGTGATGGGCTAG 792
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Search completed: May 12, 2003, 01:58:04  
Job time : 98 secs

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2003, 01:56:39 ; Search time 28 Seconds  
(without alignments)  
552.773 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MYQVAFPLAMVMTHTYSHW.....ERRLYRSLACVCVRPRVMG 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	107	11.8	162	2	T32515	hypothetical prote
2	92.5	10.2	151	1	B45351	immediate-early pr
3	91	10.0	150	2	I49623	cytotoxic T-lympho
4	86	9.5	147	2	JC4628	cytotoxic T-lympho
5	83	9.1	1323	2	I78557	N-methyl-D-asparta
6	81.5	9.0	467	2	A47388	serine/threonine p
7	80.5	8.8	422	1	A60503	sperm-binding glyco
8	78.5	8.6	206	2	T25139	hypothetical prote
9	78	8.6	358	1	J00805	hydrogenase (EC 1.
10	77	8.5	263	2	T48742	hydrogenase (EC 1.
11	77	8.5	344	1	S11776	hydrogenase (EC 1.
12	76.5	8.4	1323	2	S27224	N-methyl-D-asparta
13	75.5	8.3	446	2	G85064	hypothetical prote
14	75.5	8.3	898	2	T14764	hypothetical prote
15	75.5	8.3	1189	2	JC6118	SH2-containing ino
16	74.5	8.2	850	2	S56015	gastric mucin MUC5
17	74.5	8.2	892	2	T06818	DNA topoisomerase
18	74.5	8.2	1132	2	J03844	telomerase catalyt
19	74.5	8.2	1373	2	TE0095	gastric mucin MUC5
20	74.5	8.2	1612	2	JC5210	DNA (cytosine-5)-
21	73.5	8.1	735	2	I48101	ADAM 6 protein pre
22	73	8.0	482	2	B31795	collagen alpha 1(X
23	73	8.0	1840	2	T30250	CT1 protein - mous
24	73	8.0	3744	2	S46715	hypothetical prote
25	72.5	8.0	240	2	A39842	insulin-like growt
26	72.5	8.0	294	2	T34537	hypothetical prote
27	72.5	8.0	419	2	T19871	hypothetical prote
28	72.5	8.0	602	2	H70796	hypothetical prote
29	72.5	8.0	1188	2	JC4889	phosphatidylinosit

30 72.5 8.0 1254 1 JQ1979 structural polypro  
31 72 7.9 238 2 I48605 insulin-like growt  
32 72 7.9 360 1 S11968 hydrogenase (EC 1.  
33 72 7.9 1348 2 S27812 probable epidermal  
34 72 7.9 1348 2 A43917 probable epidermal  
35 71.5 7.9 166 2 C72734 hypothetical prote  
36 71 7.8 488 2 S13423 stromelysin 3 (EC  
37 71 7.8 564 2 T45866 hypothetical prote  
38 71 7.8 1057 2 T30638 hypothetical prote  
39 70.5 7.7 545 1 A39193 cytochrome ccs pre  
40 70.5 7.7 914 1 JN0550 iodide peroxidase  
41 70.5 7.7 3942 2 T42730 Bassoon protein -  
42 70 7.7 148 2 T21334 hypothetical prote  
43 70 7.7 479 2 AD0845 probable flavoprot  
44 70 7.7 583 1 A41129 radixin - mouse  
45 69.5 7.6 108 2 B69152 polyferredoxin - M

## ALIGNMENTS

## RESULT 1

T32515

hypothetical protein C44B12.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C:Accession: T32515

R:Tin-Wollam, A.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid C44B12.

A:Reference number: Z21183

A:Accession: T32515

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-162 <TIN>

A:Cross-references: EMBL:AF036692; PIDN:AAB88329.1; GSPDB:GN00022; CESP:C44B12.6

A:Experimental source: strain Bristol N2; clone C44B12

C:Genetics:

A:Gene: CESP:C44B12.6

A:Map position: 4

A:Introns: 41/3; 95/3; 115/1

Query Match

Best Local Similarity 11.8%; Score 107; DB 2; Length 162;

Matches 34; Conservative 23; Mismatches 39; Indels 34; Gaps 6;

Qy 27 KGQDTSELLRWSTVPVPPLEPARPNRHPESCRAEDGPLNSRAISPRVYELDRDLNRLP 86

Db 57 KSRDCSEPSIDKSSEVLP-----DQPLSERSCIPYHHILNYDEKRIP 98

Qy 87 QDLYHARCLCPHCVSLOTG-SHMDPRGNSELYHNQTVFYRRPCGKEGKTHKGVCYCLERRL 145

Db 99 AAISEVEGSCPH-VKVGHHIICPE-----MMYNRMVLFDDSC--DK-----YVERY 143

Qy 146 YRVSLACVCV 155

Db 144 QRVALACVPV 153

## RESULT 2

B45351

immediate-early protein 2 - saimirine herpesvirus 1 (strain 11)

N:Alternate names: hypothetical protein ORF13

C:Species: saimirine herpesvirus 1

A:Note: host Saimiri sciureus (common squirrel monkey)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Jul-1999

C:Accession: B45351; D36807

R:Nicholas, J.; Smith, E.P.; Coles, L.; Honess, R.

Virology 179, 189-200, 1990

A:Title: Gene expression in cells infected with gammaherpesvirus saimiri: properties

A:Reference number: A45351; MUID:91021021; PMID:1699352

A:Accession: B45351

A:Molecule type: mRNA

C;Accession: JC4628  
R.;Yao, Z.; Timour, M.; Painter, S.; Fanslow, W.; Spriggs, M.  
Gene 168, 223-225, 1996  
A;Title: Complete nucleotide sequence of the mouse CTLA8 gene;  
A;Reference number: JC4628; MUID:96194901; PMID:8654948  
A;Accession: JC4628  
A;Molecule type: DNA  
A;Residues: 1-147 <YAO>  
A;Cross-references: GB:U35108; NID:g1244499; PIDN:AAA93253.1; PID:g1244500  
C;Genetics:  
A;Gene: ctla8  
A;Introns: 69/2  
C;Superfamily: saimiri herpesvirus immediate-early protein 2  
C;Keywords: cytokine; glycoprotein; lymphocyte  
F;I-14/Domain: signal sequence #status predicted <SIG>  
F;I-14/Product: cytotoxic T-lymphocyte-associated antigen 8 #status predicted <MAT>  
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.5%; Score 86; DB 2; Length 147;  
Best Local Similarity 27.3%; Pred. No. 0.86;  
Matches 24; Conservative 16; Mismatches 40; Indels 8; Gaps 3;

Qy 68 SRATSPWRYELDRDLNLKLPDLYHARCLCPHCYSVLTGSHMDPRGNSELLVHNQTVEYRR 127  
: : | | | : | | : | | : | | : | | : |  
Db 60 NRSTSPWTLHRNEPDRLPSVINEAQRCQRVCNAE--GKLDRHMNSVLQQEILVKRE 117  
: : | | | : | | : | | : | | : | | : |

Qy 128 PCHGEKTHKGICYLERLRVSLACVCV 155  
: : | | : | | : | | : | |

Db 118 P---ESCPTFRVERKML--VGVGCTCV 139  
: : | | : | | : | | : | |

RESULT 5

I78557  
N-methyl-D-aspartate receptor chain NMDAR2D-2 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Aug-1996 #sequence.revision 02-Aug-1996 #text\_change 21-Jan-2000  
C;Accession: I78557; I58158; D45219  
R.;Monyer, H.; Burnashev, N.; Laurie, D.J.; Sakmann, B.; Seeburg, P.H.  
Neuron 12, 529-540, 1994  
A;Title: Developmental and regional expression in the rat brain and functional properties  
A;Reference number: I58158; MUID:94206533; PMID:7512349  
A;Accession: I78557  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1323 <RES>  
A;Cross-references: GB:L31612; NID:g469068; PIDN:AAC37647.1; PID:g469069  
A;Accession: I58158  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-66, 'V', 68-1323 <RE2>  
A;Cross-references: GB:L31611; NID:g469066; PIDN:AAC37646.1; PID:g469067  
R.;Biol. T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazawa, J.  
J. Biol. Chem. 268, 2836-2843, 1993  
A;Title: Molecular characterization of the family of the N-methyl-D-aspartate receptors  
A;Reference number: A45219; MUID:93155102; PMID:8428958  
A;Accession: D45219  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1265-1323 <ISH>  
A;Experimental source: brain  
A;Note: sequence extracted from NCBI backbone (NCBIP:124265)  
C;Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology  
F;451-879/domain: glutamate receptor homology <GRS>

Query Match 9.1%; Score 83; DB 2; Length 1323;  
Best Local Similarity 26.7%; Pred. No. 15;  
Matches 35; Conservative 7; Mismatches 39; Indels 50; Gaps 7;

Qy 38 WSTVPVPPLEPAR---PNRHPESCRASDGFL-----NSRAISPWRYELDRDLNLPLQ 87  
: : | | | : | | : | | : | | : | | : |

Db 1202 WAAGP-PERRARCPCRPHPHRPRASHRAPAAPHHHRRRAAGWDPPPAPTSSLE 1260  
: : | | | : | | : | | : | | : | | : |

Qy 88 DL-----YHARCLCPHCV-----SLQTGSHMDPRGNSELLVHNQTVEYRR 127

Db 1261 DLSSCPRAAPTRRLTGPSSRHAR-RCPHAAHMGPPPLPTASHRRHRG----- 1304  
QY 128 PCHGEGTHKG 138  
Db 1305 ---GDLGTRRG 1312

RESULT 6  
A47388  
serine/threonine protein kinase - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: A47388  
R:Patricotis, C.; Makris, A.; Bear, S.E.; Tschlis, P.N.  
Proc. Natl. Acad. Sci. U.S.A. 90, 2251-2255, 1993  
A:Title: Tumor progression locus 2 (tpl-2) encodes a protein kinase involved in the prog  
A:Reference number: A47388; MUID:93211939; PMID:7691591  
A:Accession: A47388  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-467 <PAT>  
A:CROSS-references: GB:M4454; NID:g207082; PIDN:AAA2185.1; PID:g207083  
A:Experimental source: liver  
A:Note: sequence extracted from NCBI backbone (NCBIN:128133, NCBI:P128134)  
C:Superfamily: protein kinase homology  
F:136-388/Domain: protein kinase homology <KIN>

Query Match 9.0%; Score 81.5; DB 2; Length 467;  
Best Local Similarity 30.3%; Pred. No. 7.1;  
Matches 33; Conservative 8; Mismatches 37; Indels 31; Gaps 5;  
QY 24 CPKSGQ--DFSEELLRWSTVPVPLEPAR-----PNRHPSCRASEDGP 65  
Db 50 CPDSNQNKHESESLR-SGQEVPLSSVRSVGTVEDLLAFANHIENKTHFRCPQESGI 108  
QY 66 LNSRAISP--WRVELDRNLRLPDLYHARCLPCHVSLQTSQSHMDPRG 112  
Db 109 LLNMVISPNQNGRYQIDSDVLLVPKLYR-----SIGSGFVPRG 147

RESULT 7  
A60503  
sperm-binding glycoprotein ZP3 precursor - golden hamster  
N:Alternate names: sperm receptor; zona pellucida glycoprotein ZP3  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A60503  
R:Kinloch, R.A.; Ruiz-Seiler, B.; Wassarman, P.M.  
Dev. Biol. 142, 414-421, 1990  
A:Title: Genomic organization and polypeptide primary structure of zona pellucida glycop  
A:Reference number: A60503; MUID:91078540; PMID:2257975  
A:Accession: A60503  
A:Molecule type: DNA  
A:Residues: 1-422 <KIN>  
A:CROSS-references: GB:M63629  
A:Note: the authors translated the codon CAA for residue 251 as Glu, and AGG for residue  
C:Comment: This sulfated glycoprotein in the zona pellucida of the oocyte is a receptor  
C:Superfamily: sperm-binding glycoprotein ZP3; ZP domain homology  
C:Keywords: glycoprotein; oocyte  
F:45-300/Domain: ZP domain homology <ZPH>

Query Match 8.8%; Score 80.5; DB 1; Length 422;  
Best Local Similarity 29.7%; Pred. No. 7.9;  
Matches 33; Conservative 14; Mismatches 37; Indels 27; Gaps 6;

QY 24 CPKSGQDTSPELLRWSTV-----PVPPLPARPNRH--PESCRASEDGPLNSRAISPWR 75  
Db 98 CSNRVQVT-EDALVYSIVLHQRPPVPGLSILRTNRADVPICRYPQGNVSSHAIRPTW 156  
QY 76 YELDRDLN-----RLPDLYHARCLCP--HC-----VSLQTSQSHM 108  
Db 157 VPFTTTSSEKLVSLRLMEENWNTKLSPTSHLGEVAVLQAEVQNGSHL 207

RESULT 8  
T25139  
hypothetical protein T22H6.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T25139  
R:McMurray, A.  
submitted to the EMBL Data Library, August 1995  
A:Reference number: Z19986  
A:Accession: T25139  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-206 <WIL>  
A:CROSS-references: EMBL:Z50797; PIDN:CAA90671.1; GSPDB:GN00028; CESP:T22H6.1  
A:Experimental source: clone T22H6  
C:Genetics:  
A:Gene: CESP:T22H6.1  
A:Map position: X  
A:Introns: 19/2; 80/3; 128/3; 162/3

Query Match 8.6%; Score 78.5; DB 2; Length 206;  
Best Local Similarity 20.0%; Pred. No. 5.8;  
Matches 33; Conservative 21; Mismatches 46; Indels 65; Gaps 6;  
QY 18 SHWPSCCP-----KQDTSSELLRWSTVPVPLEPARPNRHPSCSRA-----S 61  
Db 63 SHYSPAPSYOQALLRLQVGLKHEQITKSS-----GKCSKKLDTIS 106  
QY 62 EDGPLNSRAISPRWRVELDRNLRLPDLYHARCLPCHVSLQTSQSHMDPRGHSSELL---- 117  
Db 107 AETPLDRALCKFEVLNYPKRLPAALTEVKCSC-----PRPSKLVGKRI 153  
QY 118 -----YHNTVTVRRPCHGKTHKGYCLERRLYRVSLACV 155  
Db 154 FECEHLRYQVRVLMWDDSCN-----TFREHVETIALACIPV 189

RESULT 9  
JQ0805  
hydrogenase (EC 1.18.99.1) small chain precursor - Azotobacter vinelandii  
N:Alternate names: hydrogenlyase; [NiFe]hydrogenase  
C:Species: Azotobacter vinelandii  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 20-Apr-2000  
C:Accession: JQ0805  
R:Menon, A.L.; Stults, L.W.; Robson, R.L.; Mortenson, L.E.  
Gene 96, 67-74, 1990  
A:Title: Cloning, sequencing and characterization of the [NiFe]hydrogenase-encoding s  
A:Reference number: JQ0805; MUID:91092503; PMID:2265761  
A:Molecule type: DNA  
A:Residues: 1-358 <MEN>  
A:CROSS-references: GB:M33152; NID:g142310; PIDN:AAA82505.1; PID:g142311  
A:Experimental source: strain OP  
A:Note: part of this sequence, including the amino end of the mature protein, was con  
C:Genetics:  
A:Gene: hoxk  
C:Complex: heterodimer; large and small chain  
C:Function:  
A:Pathway: hydrogen metabolism  
A:Note: contains iron-sulfur and nickel  
C:Superfamily: hydrogenase (NiFe) small chain  
C:Keywords: 3Fe-4S; 4Fe-4S; heterodimer; hydrogen metabolism; iron-sulfur protein; me  
F:1-45/Domain: signal sequence #status predicted <SIG>  
F:46-358/Product: hydrogenase small chain #status experimental <NAT>  
F:62, 65, 160, 194/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F:232, 235, 260, 266/Binding site: 4Fe-4S cluster (His, Cys, Cys) (covalent) (type  
F:275, 294, 297/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 8.6%; Score 78; DB 1; Length 358;  
Best Local Similarity 21.9%; Pred. No. 11;  
Matches 37; Conservative 19; Mismatches 35; Indels 78; Gaps 11;

```

C:Superfamily: hydrogenase (NiFe) small chain
C:Keywords: 3Fe-4S; 4Fe-4S; heterodimer; hydrogen metabolism; iron-sulfur protein; m
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-344/Product: hydrogenase (uptake) small chain #status predicted <MAT>
F:51,54,146,180/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F:218,221,246,252/Binding site: 4Fe-4S cluster (His, Ser, Cys, Cys) (covalent) (type
F:261,280,283/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match      8.5%; Score 77; DB 1; Length 344;
Best Local Similarity 21.3%; Pred. No. 13;
Matches 36; Conservative 21; Mismatches 34; Indels 78; Gaps 11;

QY 20 WPSCCPGKQDTSSELLRNSTVPPVPLEPARNPHPSCRASEDCGPLNSRAISPRYELD 79
      |||
Db 143 WGSCA-----SMGCV-----QAAKPN-----PTQAVPIHKVITD 171
      |||
QY 80 RDLNRLPODLYHARCLCPHCVSLSQTG-----SHMDPRGNSELLY-----HNQTVF 124
      |||
Db 172 KPMKVPG-----CPPIAEVWTGVITMYLTGKLPDLRQGRPKMFYGGRIHDKS-- 221
      |||
QY 125 YRRPCH-----GEKGTGKGYCLERLYRVSL-----ACVCVR 156
      ||||
Db 222 YRRP-HFDAGQFVEHWDDEGARKGYC----LYKVGCKGPTSYNACSTVR 265
      ||||

RESULT 12
S27224
N-methyl-D-aspartate receptor epsilon-4 chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C:Accession: S27224
R:Iikeda, K.; Nagasawa, M.; Mori, H.; Araki, K.; Sakimura, K.; Watanabe, M.; Inoue, Y.
FEBS Lett. 313, 34-38, 1992
A:Title: Cloning and expression of the epsilon-4 subunit of the NMDA receptor channel
A:Reference number: S27224; MUID:93050214; PMID:1385220
A:Accession: S27224
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1323 <IKR>
A:Cross-references: EMBL:D12822
C:Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology
C:Keywords: transmembrane protein
F:451-879/Domain: glutamate receptor homology <GRH>

Query Match      8.4%; Score 76.5; DB 2; Length 1323;
Best Local Similarity 25.5%; Pred. No. 58;
Matches 35; Conservative 6; Mismatches 41; Indels 55; Gaps 7;

QY 38 WSTVVP-----PLEPAR-----PNRHPSCRASEDGPL-----NSRAISPRYELDRD 81
      |||
Db 1195 WAPPPPPWAAGPAPRRARCGCPRHPRRASHRAPAAAPHHHRRRAAGGMDLPPAP 1254
      |||
QY 82 LNRLPODL-----YHARCLCPHCV-----SLQTSGSHMDPRGNSELLYHNQ 121
      |||
Db 1255 TGRSEDLSSCPRAAPTRRLTGTSRHRAR-RCPPAAHWGCPPLTASHRRHRG----- 1304
      |||
QY 122 TVFYRRPCHGEKGTGK 138
      |||
Db 1305 -----GDLGTRRG 1312

RESULT 13
G85064
hypothetical protein AF4905150 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: G85064
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: G85064
A:Status: preliminary

```



Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	898	98.7	177	1	I17E_HUMAN	O9h293 homo sapien
2	165.5	18.2	197	1	I17C_HUMAN	Q9p0m4 homo sapien
3	125.5	13.6	180	1	I17B_HUMAN	O9ubf5 homo sapien
4	123.5	13.6	180	1	I17B_MOUSE	O9qxt6 mus musculus
5	120.5	13.2	153	1	I17F_MOUSE	O9p0pd4 homo sapien
6	116.5	12.8	178	1	I17F_HUMAN	O9eqi6 mesocricetu
7	96.5	10.6	155	1	I17I_HUMAN	O16552 homo sapien
8	92.5	10.2	151	1	VG13_HSVSA	P24916 herpesvirus
9	91	10.0	150	1	I17I_RAT	O61453 rattus norv
10	89.5	9.8	151	1	VG13_HVSC	O40633 herpesvirus
11	86	9.5	158	1	I17I_MOUSE	O62386 mus musculus
12	83	9.1	1323	1	NME4_RAT	O62645 rattus norv
13	81.5	9.0	467	1	M3K8_RAT	O63562 rattus norv
14	80.5	8.8	422	1	ZP3_MESAU	P23491 mesocricetu
15	78	8.6	358	1	MBHS_AZOVI	P21950 azotobacter
16	77.5	8.5	966	1	ST10_MOUSE	O55098 mus musculus
17	77.5	8.5	1581	1	LMG3_MOUSE	O9r0b6 mus musculus
18	77	8.5	344	1	MBHS_AZOCH	P18190 azotobacter
19	77	8.5	1050	1	TUR7_MOUSE	P58681 mus musculus
20	76.5	8.4	988	1	CHS1_EXODE	P30600 exophiala d
21	76.5	8.4	1323	1	NME4_MOUSE	O30391 mus musculus
22	76.5	8.4	1696	1	PKC5_BRACL	O9uj15 brachiosteo
23	74.5	8.2	1132	1	TEPT_HUMAN	O14746 homo sapien
24	74.5	8.2	1612	1	DNM1_PARLI	O27746 paracentrot
25	74	8.1	1336	1	NME4_HUMAN	O15399 homo sapien
26	73	8.0	482	1	CA1B_RAT	P20909 rattus norv
27	73	8.0	3744	1	YHP9_YEAST	P38811 saccharomyc
28	72.5	8.0	240	1	IBP6_HUMAN	P24592 homo sapien
29	72.5	8.0	545	1	HMWC_DESVH	P24092 desulfovibr
30	72.5	8.0	930	1	SM6C_HUMAN	O9h3t2 homo sapien
31	72.5	8.0	1254	1	POL5_EEVMY	P36331 venezuelan
32	72.5	8.0	3695	1	LMAS_HUMAN	O15230 homo sapien
33	72	7.9	238	1	IBP6_MOUSE	P47880 mus musculus



```
QY 63 DGPLNSRAISPMRYELDRDLNRLPDYHARCLCPHCYSLOTGSHMDPRGNSELYHNQT 122
DB 79 DGPLNSRAISPMRYELDRDLNRLPDYHARCLCPHCYSLOTGSHMDPRGNSELYHNQT 138
QY 123 VFYRRPCHGKTHGKCYCLERLYRVSACVVRPRVMG 161
DB 139 VFYRRPCHGKTHGKCYCLERLYRVSACVVRPRVMG 177

RESULT 2
IL17C_HUMAN
ID IL17C_HUMAN STANDARD; PRT; 197 AA.
AC Q9P0M4; Q9HC75;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Interleukin-17 precursor (IL-17C) (Cytokine CX2).
GN IL17C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20105548; PubMed=10639155;
RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,
RA Gurney A.L., Wood W.I.;
RT "Cloning and characterization of IL-17B and IL-17C, two new members
RT of the IL-17 cytokine family.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX Zhang W., He L., Wan T., Yuan Z., Cao X.;
RT "A novel human cytokine CX2 with homology to IL-17.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Stimulates the release of tumor necrosis factor alpha
CC and IL-1beta from the monocytic cell line THP-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
CC
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DR EMBL; AF152099; AAF28105.1; -
DR EMBL; AF142410; AAG27921.1; -
DR Genew; HGNC:5983; IL17C.
DR MIM; 604628; -
KW Cytokine; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 197 INTERLEUKIN-17C.
FT DISULFID 129 189 BY SIMILARITY.
FT DISULFID 134 191 BY SIMILARITY.
FT CONFLICT 50 50 H -> R (IN REF. 2).
SQ SEQUENCE 197 AA; 21765 MW; BAE0152E18DE7D08 CRC64;

Query Match 18.2%; Score 165.5; DB 1; Length 197;
Best Local Similarity 29.7%; Pred. No. 7.8e-09;
Matches 52; Conservative 16; Mismatches 37; Gaps 7;

QY 15 HTYSHWPCSCPSKQDTSSEL-----LRW-STVP---VPPLEPAPRNHPES 57
DB 27 HPISHGTPHCYIS-----AELPLGQAPPHLLARCAKNGQALPVALVSSLEAASHRGHER 81
QY 58 CRASEDGPL-----NSRAISPMRYELDRDLNRLPDYHARCLCPHCYSLOTGS 106
DB 82 PSATTQCPVLRPEVLEADTHQRSISPMRYVDTEDEYFQKLAFAECLRCGCIDANTGR 141
QY 107 HMDPRGNSELYHNQTVFYRRPCHGKGEK-----THGKCYCLERLYRVSACVVRPR 158
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DB 142 ETAAL-NSVRLQLSLVLRRRPCSRDGLPTGAFATHTFIHVPVGTCTVLPR 195

RESULT 3
IL17B_HUMAN
ID IL17B_HUMAN STANDARD; PRT; 180 AA.
AC Q9UHF5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-17B precursor (IL-17B) (Cytokine-like protein ZCYT07)
DE (Neuronal interleukin-17 related factor) (Interleukin-20).
GN IL17B OR ZCYT07 OR N1RF OR IL20.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
RA Martinez T., Hoffman R., O'Hara P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20317118; PubMed=10749887;
RA Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,
RA Barber M.C., Wang W., Wathen K., Hodge V., Fisher C.L., Olsen H.,
RA Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A.,
RA Carrell J.A., Ebner R.;
RT "A novel cytokine receptor-ligand pair. Identification, molecular
RT characterization, and in vivo immunomodulatory activity.";
RL J. Biol. Chem. 275:19167-19176(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,
RA Gurney A.L., Wood W.I.;
RT "Cloning and characterization of IL-17B and IL-17C, two new members
RT of the IL-17 cytokine family.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,
RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;
RT "Identification of a novel IL-17 related factor: demonstration of
RT neuronal expression and evaluation as a candidate for the chromosome
RT 5q-linked form of Charcot-Marie-Tooth disease.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX Zhang W., Wang J., Cao X.;
RL "Novel cytokine homology with interleukin-17.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Stimulates the release of tumor necrosis factor alpha
CC and IL-1beta from the monocytic cell line THP-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in adult pancreas, small intestine,
CC prostate, colon mucosal lining, and ovary.
CC -!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
CC
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Db      140 VSVGCTCTPTV 151

RESULT 8
VG13_HSVSA STANDARD; PRT; 151 AA.
ID      VG13_HSVSA
AC      P24916;
DT      01-MAR-1992 (Rel. 21, Created)
DT      01-MAR-1992 (Rel. 21, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Immediate early gene 13 protein precursor.
GN      13 OR KCLF2.
OS      Herpesvirus saimiri (strain 11).
OC      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC      Gammaherpesvirinae; Rhadinovirus.
OX      NCBI_TaxID=10383;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=90163221; PubMed=2154888;
RA      Albrecht J.-C., Fleckenstein B.;
RT      "Structural organization of the conserved gene block of Herpesvirus
RT      saimiri coding for DNA polymerase, glycoprotein B, and major DNA
RT      binding protein.";
RL      Virology 174:533-542(1990).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92333688; PubMed=1321287;
RA      Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
RA      Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
RA      Honess R.W.;
RT      "Primary structure of the herpesvirus saimiri genome.";
RL      J. Virol. 66:5047-5058(1992).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=91021021; PubMed=1699352;
RA      Nicholas J., Smith E.P., Coles L., Honess R.;
RT      "Gene expression in cells infected with gammaherpesvirus saimiri:
RT      properties of transcripts from two immediate-early genes.";
RL      Virology 179:189-200(1990).
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
-----
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DR      EMBL; X64346; CAA45636.1; -
DR      EMBL; M31122; AAA46169.1; -
DR      EMBL; M60286; AAA46156.1; -
DR      PIR; D36807; D36807.
DR      PIR; B45351; B45351.
DR      Cytokine; Early protein; Signal.
FT      SIGNAL 1 22 POTENTIAL.
FT      CHAIN 23 151 IMMEDIATE EARLY GENE 13 PROTEIN.
FT      DISULFID 90 140 BY SIMILARITY.
FT      DISULFID 95 142 BY SIMILARITY.
FT      CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE 151 AA; 17180 MW; 53BDEDE4206C432 CRC64;
Query Match 10.2%; Score 92.5; DB 1; Length 151;
Best Local Similarity 27.7%; Pred. No. 0.047;
Matches 31; Conservative 19; Mismatches 43; Indels 19; Gaps 5;

Qy      52 NRHPESCRAEDGPNLSRAISPMRYELDRDLNRPDQYLHARCILCPHCYSVLTQGSMDPR 111
Db      51 NWNTSSKRASD---VYNRSTSPWTLRHNEODDQRPVSVIWEAKRCYGLCNVAD----- 99

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FT DOMAIN 278 283 POLY-GLY.
FT DOMAIN 905 913 POLY-PRO.
FT DOMAIN 1030 1035 POLY-ALA.
FT DOMAIN 1197 1201 POLY-PRO.
FT SITE 639 639 FUNCTIONAL DETERMINANT OF NMDA
RECEPTORS (BY SIMILARITY).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 349 349 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 464 464 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 566 566 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1265 1323 CPAAATRLTGSRHRCRPHAAHGHPPLPTASHRRHGG
DLGTRGSAHFSLESEV -> RCPDPRHTGDTGAGTWAHA
GALRISPAWSPRYDAAPPTTPAAPSAGHGPRGRKWT
GPSWVGKDRNGPGRTPPGAASCAPTPEALGEL (IN
ISOFORM 1).
FT CONFLICT 25 25 A -> V (IN REF. 3).
FT CONFLICT 47 47 P -> Q (IN REF. 3).
FT CONFLICT 67 67 G -> V (IN REF. 2; AAC37646).
FT CONFLICT 94 94 R -> P (IN REF. 2).
FT CONFLICT 305 305 R -> A (IN REF. 2).
FT CONFLICT 635 635 A -> G (IN REF. 3).
FT CONFLICT 974 974 E -> D (IN REF. 3).
FT CONFLICT 1253 1253 A -> G (IN REF. 3).
FT CONFLICT 1266 1267 PR -> TT (IN REF. 3).
SQ SEQUENCE 1323 AA; 143100 MW; 40F7D60192579564 CRC64;

Query Match 9.1%; Score 83; DB 1; Length 1323;
Best Local Similarity 26.7%; Pred. No. 4;
Matches 35; Conservative 7; Mismatches 39; Indels 50; Gaps 7;

QY 38 WSTVPVPLEPAR---PNRHPSCRASEDGPL-----NSRAISPWRYELDRDLNRLPQ 87
| : | | | | | | | | | : | | : | : |
DB 1202 WAAGP-PPRRRCGCGPRPHPRASHRAPAAAPHHRRAAGGWDFPPAPTARSLE 1260

QY 88 DL-----YHARCLPCV-----SLQSGHMDPRGNSLLYHNTVYRR 127
| | | | | | | | | | | | | | | |
DB 1261 DLSSCPAAATRLTGSPRSHAR-RCPHAAHWGPLPTASHRRHG----- 1304

QY 128 PCHGKGTGK 138
| : | : |
DB 1305 --GDLGTRG 1312

RESULT 13
M3K8_RAT
ID M3K8_RAT STANDARD; PRT; 467 AA.
AC Q63562;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitogen-activated protein kinase kinase 8 (EC 2.7.1.-) (Tumor
progression locus 2) (TPL-2).
GN MAP3K8 OR TPL2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Long Evans; TISSUE=Liver;
RA MEDLINE=93211939; PubMed=7681591;
RX Patriotic C., Makris A., Bear S.E., Tschlis P.N.;
RT "Tumor progression locus 2 (Tpl-2) encodes a protein kinase involved
in the progression of rodent T-cell lymphomas and in T-cell
activation.";
RT Proc. Natl. Acad. Sci. U.S.A. 90:2251-2255(1993).
RN [2]
RP FUNCTION, AND MAP3K8-NFKB1/PI05 BINDING.
RX MEDLINE=99133929; PubMed=9950430;
RA Belich M.P., Salmeron A., Johnston L.H., Ley S.C.;
RT "TPL-2 kinase regulates the proteolysis of the NF-kappaB-inhibitory
protein NF-kappaB1 p105.";

```

```

RL Nature 397:363-368(1999).
CC -I- FUNCTION: Able to activate NF-kappa-B 1 by stimulating proteasome-
mediated proteolysis of NF-kappa-B 1/p105. Plays a role in the
cell cycle.
CC -I- SUBUNIT: Interacts with NFKB1/PI05.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- TISSUE SPECIFICITY: Expressed in spleen, thymus, liver and lung.
CC -I- PTM: Autophosphorylated.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
CC EMBL; M94454; AAA2185.1; .
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR Transferase; Serine/threonine-protein kinase; Proto-oncogene;
KW ATP-binding; Phosphorylation.
FT DOMAIN 146 388 PROTEIN KINASE.
FT NP_BIND 144 152 ATP (BY SIMILARITY).
FT BINDING 167 167 ATP (BY SIMILARITY).
FT ACT_SITE 253 253 BY SIMILARITY.
SQ SEQUENCE 467 AA; 52807 MW; 454E0E32768A4BD CRC64;

Query Match 9.0%; Score 81.5; DB 1; Length 467;
Best Local Similarity 30.3%; Pred. No. 1.8;
Matches 33; Conservative 8; Mismatches 37; Indels 31; Gaps 5;

QY 24 CPSKQ--DTSEELLRWSTVPVPLEPAR-----PNRHPSCRASEDGP 65
| : | | | | | | | | | : | | | |
DB 50 CPDSNQNKHESELLR-SGQEVPLSSVRYGVEDLLAFANHISNTKHFYRCPOESGI 108

QY 66 LNSRAISP--WRYELDRDLNRLPDQLYHARCLPCVSLQSGHMDPRG 112
| : | | | | | | | | | : | | |
DB 109 LLNMVISPNQNGRYQIDSVLLVPWKLTYR-----SIGSGFVPRG 147

RESULT 14
ZP3_MESAU
ID ZP3_MESAU STANDARD; PRT; 422 AA.
AC P23491;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Zona pellucida sperm-binding protein 3 precursor (Zona pellucida
glycoprotein zp3) (Sperm receptor) (Zona pellucida protein C).
GN ZP3.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OC NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE=91078540; PubMed=2257975;
RA Kinloch R.A., Ruiz-Seller B., Wassarman P.M.;
RT "Genomic organization and polypeptide primary structure of zona
pellucida glycoprotein hzp3, the hamster sperm receptor.";
RL Dev. Biol. 142:414-421(1990).
CC -I- FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSIBLE FOR
SPERM-ADHESION TO THE ZONA PELLUCIDA, AND MAY CONTRIBUTE TO THE

```





GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 12, 2003, 01:55:24 ; Search time 45 Seconds  
(without alignments)  
737.191 Million cell updates/sec

Title: US-10-037-591a-2

Perfect score: 910

Sequence: 1 MYQVAFVFLAMVGMGTHTYSHW.....ERRLYRSLACVCRPRVMG 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organellae.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	904	99.3	161	Q8WXB0	Q8vhh8 homo sapien
2	709	77.9	169	Q8VHH8	Q8vhh8 mus musculu
3	652	71.6	153	Q8VHC9	Q8vhh9 mus musculu
4	126.5	13.9	202	Q8TAD2	Q8tad2 homo sapien
5	114	12.5	111	Q9BQI7	Q9eqi7 rattus norv
6	107	11.8	162	5	Q44146 caenorhabdi
7	95	10.4	141	6	Q95156 bos taurus
8	87	9.6	499	5	Q9GZ34 trypanosoma
9	83	9.1	405	4	Q9BU21 homo sapien
10	81	8.9	1394	5	Q9VS89 Q9vs89 drosophila
11	80.5	8.8	379	13	Q9NKKZ8 Q9nkz8 eptaretus
12	78.5	8.6	174	10	Q8RVH7 Q8rvh7 populus tre
13	78.5	8.6	206	5	Q22687 Q22687 caenorhabdi
14	78	8.6	459	11	Q9DC55 Q9dc55 mus musculu
15	78	8.6	459	11	Q9D624 Q9d624 mus musculu
16	78	8.6	459	11	Q9CXA8 Q9cxa8 mus musculu

17	78	8.6	1090	10	Q8S1E5	Q8s1e5 oryza sativ
18	76.5	8.4	1615	11	Q9JIR4	Q9jir4 ratus norv
19	76	8.4	2434	10	Q94JB3	Q94jb3 oryza sativ
20	75.5	8.3	272	12	Q36279	Q36279 venezuelan
21	75.5	8.3	272	12	Q36281	Q36281 venezuelan
22	75.5	8.3	289	12	Q9QAT3	Q9qat3 venezuelan
23	75.5	8.3	289	12	Q9QAT2	Q9qat2 venezuelan
24	75.5	8.3	289	12	Q9QAT1	Q9qat1 venezuelan
25	75.5	8.3	289	12	Q9QAT0	Q9qat0 venezuelan
26	75.5	8.3	289	12	Q9QAS9	Q9qas9 venezuelan
27	75.5	8.3	289	12	Q9QAS8	Q9qas8 venezuelan
28	75.5	8.3	289	12	Q9QAS7	Q9qas7 venezuelan
29	75.5	8.3	289	12	Q9QAS6	Q9qas6 venezuelan
30	75.5	8.3	289	12	Q9QAS5	Q9qas5 venezuelan
31	75.5	8.3	289	12	Q9QAS4	Q9qas4 venezuelan
32	75.5	8.3	289	12	Q9YJBI	Q9yjb1 venezuelan
33	75.5	8.3	289	12	Q9W9J3	Q9w9j3 venezuelan
34	75.5	8.3	334	5	Q961F6	Q961f6 drosophila
35	75.5	8.3	369	5	Q8SUP9	Q8sup9 encephalito
36	75.5	8.3	432	4	Q9NPM2	Q9nrm2 homo sapien
37	75.5	8.3	446	10	Q9M0Y0	Q9m0y0 arabidopsis
38	75.5	8.3	477	10	Q94ON7	Q94on7 arabidopsis
39	75.5	8.3	867	11	Q9JLF9	Q9jlf9 mus musculu
40	75.5	8.3	874	5	Q9VSE3	Q9vse3 drosophila
41	75.5	8.3	883	5	Q8SX53	Q8sx53 drosophila
42	75.5	8.3	898	4	Q9UFZ4	Q9ufz4 homo sapien
43	75.5	8.3	928	11	Q9JLGO	Q9jlg0 mus musculu
44	75.5	8.3	1130	11	Q9WUC2	Q9wuc2 mus musculu
45	75.5	8.3	1190	11	Q9ES52	Q9es52 mus musculu

## ALIGNMENTS

### RESULT 1

Q8WXB0	PRELIMINARY;	PRT;	161 AA.
AC	Q8WXB0;		
DT	01-MAR-2002 (TREMBLrel. 20, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	IL25.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
EX	MEDLINE=21629216; PubMed=11754819;		
RA	Fort M.M., Cheung J., Yen D., Li J., Zurawski S.M., Lo S., Menon S.,		
RA	Clifford T., Hunte B., Lesley R., Muchamuel T., Hurst S.D.,		
RA	Zurawski G., Leach M.W., Gorman D.M., Rennick D.M.;		
RT	"IL-25 Induces IL-4, IL-5, and IL-13 and Th2-Associated Pathologies In Vivo."		
RL	Immunity 15:985-995(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Hurst S.D., Muchamuel T., Gorman D.M., Gilbert J.M., Clifford T.,		
RA	Kwan S., Menon S., Seymour B., Jackson C., Kung T., Brieland J.,		
RA	Zurawski S.M., Chapman R., Zurawski G., Coffman R.L.;		
RT	"New IL-17 family members promote Th1 or Th2 responses in the lung: In vivo function of the novel cytokine IL-25."		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF458059; AAL57622.1;		
SQ	SEQUENCE 161 AA; 18537 MW; 32C85913FCFE151D CRC64;		

Query Match 99.3%; Score 904; DB 4; Length 161;

Best Local Similarity 100.0%; Pred. No. 1.1e-89;

Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYQVAFVFLAMVGMGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPPLEPRNHPSCRA 60

Db 1 MYQVAFVFLAMVGMGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPPLEPRNHPSCRA 60

```
Qy 61 SEDGPLNSRAISPRYELDRDLNRLPDLYHARCLPCHVSLQTSQSHMDPRGNSSELLVHN 120
|||||
Db 61 SEDGPLNSRAISPRYELDRDLNRLPDLYHARCLPCHVSLQTSQSHMDPRGNSSELLVHN 120
|||||
Qy 121 QTVFYRRPCHGEGKTHGKCYCLRLRYRSLACVCRPRVM 160
|||||
Db 121 QTVFYRRPCHGEGKTHGKCYCLRLRYRSLACVCRPRVM 160
|||||

RESULT 2
Q8VHH8
ID Q8VHH8 PRELIMINARY; PRT; 169 AA.
AC Q8VHH8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE IL25.
GN IL17E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; PubMed=11754819;
RX Fort M.M., Cheung J., Yen D., Li J., Zurawski S.M., Lo S., Menon S.,
RA Clifford T., Hunte B., Lesley R., Muchamuel T., Hurst S.D.,
RA Zurawski G., Leach M.W., Gorman D.M., Rennick D.M.;
RT "IL-25 Induces IL-4, IL-5, and IL-13 and Th2-Associated Pathologies in
RT Vivo.";
RL Immunity 15:985-995(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX Hurst S.D., Muchamuel T., Gorman D.M., Gilbert J.M., Clifford T.,
RA Kwan S., Menon S., Seymour B., Jackson C., Kung T., Brieland J.,
RA Zurawski S.M., Chapman R., Zurawski G., Coffman R.L.;
RT "New IL-17 family members promote Th1 or Th2 responses in the lung: In
RT vivo function of the novel cytokine IL-25.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458060; AAL57623.1;
DR MGD; MGI:2155888; IL17E.
SQ SEQUENCE 169 AA; 19210 MW; CFAD2CEDE452C94D CRC64;

Query Match 77.9%; Score 709; DB 11; Length 169;
Best Local Similarity 76.8%; Pred. No. 1.2e-68;
Matches 129; Conservative 9; Mismatches 22; Indels 8; Gaps 1;

Qy 1 MYQVAFIAMVGTHTVSLRTOECSHLPSCPSKEQPEEWLKNSSASVSPPEPLSHT 60
|||||
Db 1 MYQVAFIAMVGTHTVSLRTOECSHLPSCPSKEQPEEWLKNSSASVSPPEPLSHT 60
|||||

Qy 53 RHPSCRASEDGPLNSRAISPRYELDRDLNRLPDLYHARCLPCHVSLQTSQSHMDPRG 112
|||||
Db 61 HHAESCRASKDGPLNSRAISPRYELDRDLNRLPDLYHARCLPCHVSLQTSQSHMDPLG 120
|||||

Qy 113 NSSELLYHNOTVYRRPCHGEGKTHGKCYCLRLRYRSLACVCRPRVM 160
|||||
Db 121 NSVPLYHNOTVYRRPCHGEGKTHGKCYCLRLRYRSLACVCRPRVM 168
|||||

RESULT 3
Q8VHC9
ID Q8VHC9 PRELIMINARY; PRT; 153 AA.
AC Q8VHC9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Interleukin 17E (Fragment).
GN IL17E.
OS Mus musculus (Mouse).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21571724; PubMed=11714825;
RA Pan G., French D., Mao W., Maruoka M., Risser P., Lee J., Foster J.,
RA Aggarwal S., Nicholes K., Guillet S., Schow P., Gurney A.B.;
RT "Forced Expression of Murine IL-17E Induces Growth Retardation,
RT Jaundice, a Th2-Biased Response, and Multiorgan Inflammation in
RT Mice.";
RL J. Immunol. 167:6559-6567(2001).
DR EMBL; AY034088; AAK59816.1;
DR MGD; MGI:2155888; IL17E.
FT NON_TER 1
SQ SEQUENCE 153 AA; 17456 MW; A0BE897842E6EB39 CRC64;

Query Match 71.6%; Score 652; DB 11; Length 153;
Best Local Similarity 81.1%; Pred. No. 1.5e-62;
Matches 116; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 18 SHWPCPCPSKGGDTSEELLRWSTVPPPLEPARPNRHPSCRASEDGPLNSRAISPRY 77
|||||
Db 10 SHLPCSCPSKEQPEEWLKNSSASVSPPEPLSHTHAESCRASKDGPLNSRAISPR 69
|||||

Qy 78 LDRDLNRLPDLYHARCLPCHVSLQTSQSHMDPRGNSSELLYHNOTVYRRPCHGEGKTHK 137
|||||
Db 70 LDRDLNRLPDLYHARCLPCHVSLQTSQSHMDPLGNSVPLVYHNOTVYRRPCHGEGKTHR 129
|||||

Qy 138 GYCLERRLRYRSLACVCRPRVM 160
|||||
Db 130 HYCLERRLRYRSLACVCRPRVM 152
|||||

RESULT 4
Q8TAD2
ID Q8TAD2 PRELIMINARY; PRT; 202 AA.
AC Q8TAD2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Interleukin 27 precursor (IL17D precursor).
GN IL27.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ENTIRE BRAIN;
RA Hadj-Slimane R., Bobe P.;
RT "Interleukin 27 (IL27): a newly identified cytokine.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hromas R.A., Starnes T.T.;
RT "IL-17D, A Novel Member of the IL-17 Family, Stimulates Cytokine
RT Production and Inhibits Hematopoiesis.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY078238; AAL6911.1;
DR EMBL; AF479775; AAM12734.1;
FT SIGNAL.
FT SIGNAL 1
SQ SEQUENCE 202 AA; 21893 MW; D171C5FB2DD039C3 CRC64;

Query Match 13.9%; Score 126.5; DB 4; Length 202;
Best Local Similarity 27.0%; Pred. No. 9e-06;
Matches 44; Conservative 17; Mismatches 69; Indels 33; Gaps 6;

Qy 20 WPCSCPSKGGQ-----DTSEELLR-----WSTVPPPLEPARPNRHP 56
|||||
Db 14 WAAGAPRAGRPARPRGCAADRPPELLEQLYGLAAGVLSAFHHHTLQLGPREQARNASCPA 73
|||||
```



01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
DE Hypothetical 55.5 kDa protein.  
OS Trypanosoma cruzi.  
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5693;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Andersson B.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF242860; AAF98145.1; -;  
KW Hypothetical protein  
SQ SEQUENCE 499 AA; 55486 MW; 6727C831B8425296 CRC64;  
Query Match 9.6%; Score 87; DB 5; Length 499;  
Best Local Similarity 28.3%; Pred. No. 0.44;  
Matches 32; Conservative 14; Mismatches 33; Indels 34; Gaps 6;  
QY 21 PSCPSKQGT---SEELRWSTVPVPLPAPRNRIPESCR-----ASEDGPLN----- 67  
DB 234 PSSPSPSGDFTSRMOKLIRKQSIPIPARHGE-KREPETDROHLGCGSETFLNSGRHP 292  
QY 68 ----SRAISPRWYELDRDLNRLPODLVHARCLCPHCVCVSLQTSQSHMDRGNSEL 116  
DB 293 SQSSSRVLSS-----SPSPNDVFHD-----TPIQSLGHSGRGYSIEI 329  
RESULT 9  
Q9BU21 PRELIMINARY; PRT; 405 AA.  
AC Q9BU21  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE Similar to hypothetical protein FLJ10101.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RC TISSUE=SKIN;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC002945; AAH02945.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 405 AA; 44298 MW; 6C30D7F7B60DBE68 CRC64;  
Query Match 9.1%; Score 83; DB 4; Length 405;  
Best Local Similarity 24.3%; Pred. No. 0.95;  
Matches 44; Conservative 10; Mismatches 51; Indels 76; Gaps 9;  
QY 39 STVPVPLEPARNRHPESCRAEDGPNLSRAI---SPWRYELDRDLNRLPQ----- 87  
DB 217 SVPPVPPE-ALP---PPACPSA---PAPRNSIISRPPFWGWRKLGALGRGQWPPWGGG 269  
QY 88 -----DLYHARCLCP----- 97  
DB 270 RACHCLGRHPLVYHRLCRCPVAACVASELEBAGHWSFGWALQVLGLQACEPALQEGRG 329  
QY 98 HCVSLQTSQSHMDRGNSELVYHNQTVYRRCPEKGHKGYCYCLERRLYRSLACVCPVR 157  
DB 330 QLASARLGGHPGGLG-----AEPVFLRDVTEAQEGPVR-VCLQ-RLGRGLAVGCALP 381  
QY 158 R 158  
DB 382 R 382  
RESULT 10  
Q9V589 PRELIMINARY; PRT; 1394 AA.  
ID Q9V589  
AC Q9V589;  
SQ SEQUENCE 1394 AA; 152269 MW; CD29380E3162F68A CRC64;

Query Match 8.9%; Score 81; DB 5; Length 1394;  
Best Local Similarity 26.5%; Pred. No. 6.2;  
Matches 27; Conservative 8; Mismatches 41; Indels 26; Gaps 5;  
QY 56 ESCRASEGPNLSRAISPRVYELDRNLRLPODLYHARCLCPHCYSVLSQTGSHMDPRGNSE 115  
DB 322 DSCTDLNPNLN-----RTRCAHECQDLPEGSY--RCVCPKGYELSEDQH----- 364  
QY 116 LLYHNQTVFYRRPCHGKGTGK---CYCLRLRYVSLACVC 154  
DB 365 -----SCLVQSPCSTKGVKCSPTGLASE-DNTSFSCIC 400  
RESULT 11  
Q9NKZ8 PRELIMINARY; PRT; 379 AA.  
AC Q9NKZ8; 379 AA.  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE HqTPN3 protein (Fragment).  
GN HqTPN3.  
OS Eptatretus burgeri (Inshore hagfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;  
OC Myxiniidae; Eptatretinae; Eptatretus.  
OX NCBI\_TaxID=7764;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2019325; PubMed=10754074;  
RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;  
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:  
RT divergence of tissue-specific isoform genes in the early evolution of  
RT vertebrates."; 50:302-311(2000).  
RL J. Mol. Evol. 50:302-311(2000).  
DR EMBL; AB033579; BAA95186.1; -.  
DR HSSP; P18031; 2HNQ.  
DR InterPro; IPR000340; DS\_phosphatase.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 1.  
DR PRINTS; PR00700; PTRYPHPTASE.  
DR SMART; SM00194; PTPC; 1.  
DR SMART; SM00012; PTPC\_DSPC; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
KW Hydrolase.  
FT NON\_TER  
FT 1  
SQ SEQUENCE 379 AA; 42672 MW; A2493B3FF3D90174 CRC64;  
Query Match 8.8%; Score 80.5; DB 13; Length 379;  
Best Local Similarity 28.0%; Pred. No. 1.6;  
Matches 33; Conservative 9; Mismatches 45; Indels 31; Gaps 6;  
QY 6 AFLAWVGTHTYSHWSPCCPSKG-----QDTSEELLRW-----STVPVPLEP--- 48  
DB 166 SFLAIQGMHLLS--ADACGQEGYLDDEENNSPEWPFYAFPPSPSTPPPPPPPKR 223  
QY 49 --ARPNNRHP-----ESCRASEGPNLS--RAISPRVYELDRNLRLPODLYHARC 94  
DB 224 STERNPGPAEAKSMWVEDLTOTELFPDNRDYELSSPTRYEFKLDGRCVDEAFGERC 281  
RESULT 12  
Q8RVH7 PRELIMINARY; PRT; 174 AA.  
AC Q8RVH7; 174 AA.  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Aux/IAA protein.  
GN IAA3.

OS Populus tremula x Populus tremuloides.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Malpighiales; Salicaceae; Populus.  
OX NCBI\_TaxID=47664;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=CAMBIAL REGION;  
RA Schrader J., Moyle R., Stenberg A., Olsson O., Sandberg G.,  
RA Bhalarao R.P.;  
RT "Aux/IAA genes and wood formation.";  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ306826; CAC84707.1; -.  
SQ SEQUENCE 174 AA; 19323 MW; 44D6FAC465BC1940 CRC64;  
Query Match 8.6%; Score 78.5; DB 10; Length 174;  
Best Local Similarity 27.2%; Pred. No. 1.1;  
Matches 28; Conservative 15; Mismatches 35; Indels 25; Gaps 5;  
QY 32 SEELLRWSTVPVPPLEPARPNRHPESCRASEDGPNLSRAISPRY----ELDRNLRLPQ 87  
DB 56 SEQLLDW-----PPKPS-----PGKAVTSENEYSSSTLFVKVYMEGIOIGRKLNLAAH 105  
QY 88 DLYHARCLCPHCYSVLSQTGSHMDPRGNSELVYHNQTVFYRRPCH 130  
DB 106 DGYHD-----LIQT---LQDMFNTSILWPEDVHESCKCH 137  
RESULT 13  
Q22687 PRELIMINARY; PRT; 206 AA.  
AC Q22687;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE T22H6.1 protein.  
GN T22H6.1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA McMurray A.A.;  
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
RT investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL; Z50797; CAA90671.1; -.  
SQ SEQUENCE 206 AA; 23959 MW; 2BDBA0A61ED7C7D2 CRC64;  
Query Match 8.6%; Score 78.5; DB 5; Length 206;  
Best Local Similarity 20.0%; Pred. No. 1.4;  
Matches 33; Conservative 21; Mismatches 46; Indels 65; Gaps 6;  
QY 18 SHWSPCCPS-----KGQDTSEELLRWSTVPVPPLEPARPNRHPESCRA-----S 61  
DB 63 SHYSPIAFSYQALLRLQVKGKLGHEQITKSS-----GKCNKKLDTIS 106  
QY 62 EDGPNLSRAISPRVYELDRNLRLPODLYHARCLCPHCYSVLSQTGSHMDPRGNSEL--- 117  
DB 107 AETPLDRALCKFEVLYNPNKRLPAALTEVKCSC-----FRPNKLVGKRI 153  
QY 118 -----YHNQTVFYRRPCHGKGTGKGYCLRLRYVSLACVCV 155  
DB 154 FECEHLRYQVRVLMWDDSCN-----TFREHVVETIALACIPV 189  
RESULT 14

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Q9DC55
ID Q9DC55 PRELIMINARY; PRT; 459 AA.
AC Q9DC55;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 1200003C23R1k protein.
GN 1200003C23R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=LUNG;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK014681; BAB29502.1; -.
DR HSP; P00743; ICCF.
DR MGD; MGI:1914114; 1200003C23R1k.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00008; EGF; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00059; lectin_c; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 1.
SQ SEQUENCE 459 AA; 49053 MW; 6CB25D048A456A7B CRC64;

Query Match 8.6%; Score 78; DB 11; Length 459;
Best Local Similarity 25.4%; Pred. No. 3.8;
Matches 34; Conservative 12; Mismatches 44; Indels 44; Gaps 7;

QY 32 SEELLRWSTVP-----VPPLEPARPNR--HPESCRASEDGLNSRAISPWRVYELDRDLN 83
DB 87 SKDLLFWVALERSISQCTQKEPLRGFSWLHPDS-EDSEDSPL-----PWVEEPQRS-- 137
QY 84 RLPDLYHARCLCPHCVSLSQTGSHMDPRGNSSELYHNQTVFYRRPCHEKGTGKCYCLER 143
DB 138 -----CTVRKCAALQATRGVEPAGWKEMRCHLRT-----DGYLCK- 172
QY 144 RLYRVSLACVCRP 157
DB 173 --YQFEVLCAPRP 184

RESULT 15
Q9D624 PRELIMINARY; PRT; 459 AA.
ID Q9D624
AC Q9D624;

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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 1200003C23R1k protein.
GN 1200003C23R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=HEAD;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK014681; BAB29502.1; -.
DR HSP; P00743; ICCF.
DR MGD; MGI:1914114; 1200003C23R1k.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00008; EGF; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00059; lectin_c; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 1.
SQ SEQUENCE 459 AA; 49065 MW; A257B38DA598EC8A CRC64;

Query Match 8.6%; Score 78; DB 11; Length 459;
Best Local Similarity 25.4%; Pred. No. 3.8;
Matches 34; Conservative 12; Mismatches 44; Indels 44; Gaps 7;

QY 32 SEELLRWSTVP-----VPPLEPARPNR--HPESCRASEDGLNSRAISPWRVYELDRDLN 83
DB 87 SKDLLFWVALERSISQCTQKEPLRGFSWLHPDS-EDSEDSPL-----PWVEEPQRS-- 137
QY 84 RLPDLYHARCLCPHCVSLSQTGSHMDPRGNSSELYHNQTVFYRRPCHEKGTGKCYCLER 143
DB 138 -----CTVRKCAALQATRGVEPAGWKEMRCHLRT-----DGYLCK- 172
QY 144 RLYRVSLACVCRP 157
DB 173 --YQFEVLCAPRP 184

Search completed: May 12, 2003, 02:00:42
Job time : 47 secs

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GenCore version 5.1.4.p5\_4578  
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## OM protein - protein search, using sw model

Run on: May 12, 2003, 01:59:09 ; Search time 23 Seconds  
(without alignments)  
205.960 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MYQVAFLANVMGHTYSHW.....ERRLYRSLACVCRPRVMG 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	13.3	205	4	US-09-724-864-37
2	120.5	13.2	153	1	US-08-514-014-12
3	120.5	13.2	153	2	US-08-833-823-12
4	120.5	13.2	163	3	US-09-034-810-2
5	120.5	13.2	163	3	US-08-685-239-2
6	96.5	10.6	155	4	US-08-432-994A-8
7	92.5	10.2	151	2	US-08-620-694A-8
8	92.5	10.2	151	3	US-09-034-810-6
9	92.5	10.2	151	3	US-09-022-255-8
10	92.5	10.2	151	3	US-08-022-696-8
11	92.5	10.2	151	3	US-08-685-239-6
12	92.5	10.2	151	3	US-09-022-253-8
13	92.5	10.2	151	3	US-09-022-260-8
14	92.5	10.2	151	4	US-09-022-259-8
15	92.5	10.2	151	4	US-09-022-257-8
16	92.5	10.2	151	4	US-08-432-994A-4
17	91	10.0	150	3	US-09-034-810-4
18	91	10.0	150	3	US-08-685-239-4
19	91	10.0	150	4	US-08-432-994A-2
20	86	9.5	158	2	US-08-620-694A-7
21	86	9.5	158	3	US-09-022-255-7
22	86	9.5	158	3	US-09-022-696-7
23	86	9.5	158	3	US-09-022-253-7
24	86	9.5	158	3	US-09-022-260-7
25	86	9.5	158	4	US-09-022-259-7
26	86	9.5	158	4	US-09-022-257-7
27	86	9.5	158	4	US-08-432-994A-10

28 76.5 8.4 1323 1 US-08-026-138E-4 Sequence 4, Appli  
29 75.5 8.3 1185 4 US-08-664-962B-2 Sequence 2, Appli  
30 75.5 8.3 1185 4 US-09-311-743-2 Sequence 2, Appli  
31 74.5 8.2 514 4 US-08-974-549A-605 Sequence 605, App  
32 74.5 8.2 807 4 US-08-974-549A-5 Sequence 5, Appli  
33 74.5 8.2 1132 3 US-08-851-843A-225 Sequence 225, App  
34 74.5 8.2 1132 4 US-08-974-549A-2 Sequence 2, Appli  
35 74.5 8.2 1132 4 US-08-974-549A-344 Sequence 344, App  
36 74.5 8.2 1132 4 US-08-854-050-225 Sequence 225, App  
37 74.5 8.2 1132 4 US-09-430-323-225 Sequence 225, App  
38 74.5 8.2 1132 4 US-09-128-354-2 Sequence 2, Appli  
39 74.5 8.2 1132 4 US-09-675-321-2 Sequence 2, Appli  
40 74.5 8.2 1132 4 US-09-052-919-2 Sequence 2, Appli  
41 74.5 8.2 1154 4 US-08-974-549A-611 Sequence 611, App  
42 74.5 8.2 1189 4 US-08-974-549A-613 Sequence 613, App  
43 74.5 8.2 1200 4 US-08-974-549A-612 Sequence 612, App  
44 74.5 8.2 1285 4 US-08-974-549A-600 Sequence 600, App  
45 74.5 8.2 1407 4 US-08-974-549A-628 Sequence 628, App

## ALIGNMENTS

## RESULT 1

US-09-724-864-37

; Sequence 37, Application US/09724864

; Patent No. 6380362

; GENERAL INFORMATION:

; APPLICANT: Watson, James D

; APPLICANT: Murison, James G.

; TITLE OF INVENTION: Polynucleotides, polypeptides expressed

; TITLE OF INVENTION: by the polynucleotides and methods for their use.

; FILE REFERENCE: 11000.1050U1

; CURRENT APPLICATION NUMBER: US/09/724,864

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678

; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 37

; LENGTH: 205

; TYPE: PRT

; ORGANISM: Mouse

US-09-724-864-37

Query Match 13.3%; Score 121; DB 4; Length 205;

Best Local Similarity 27.1%; Pred. No. 1.2e-05;

Matches 42; Conservative 19; Mismatches 58; Indels 36; Gaps 7;

QY 25 PSKQDTSLELR-----WSTVPVPPLEPAPRPNRHPSCRASE---DGPLN 67

DB 35 PRDCADRPPELLEQLYGRLAAGVLSAFHHTLQLGPREQARNASCAGGAADRRFRPPTN 94

QY 68 SRAISPWRYELDRDLNRLPDLYHARCLPHCVSLTGTSHMDPRGNSLLYHNOTVF--- 124

DB 95 LRSVFWAYRISYDPAFPYLPPEAYCLRGCL---TGLY----GEDFRFRSTPVPSP 147

QY 125 --YRR--PCHGKGTGKHYGLRRLRYRSLACVCV 155

DB 148 VVLRRTACAGGRSVYAEHVI-----TIPVGTCV 177

## RESULT 2

US-08-514-014-12

; Sequence 12, Application US/08514014

; Patent No. 5707829

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; APPLICANT: McCoy, John

; APPLICANT: Kelleher, Kerry

; APPLICANT: Carlin, McKough

; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS

; TITLE OF INVENTION: ENCODED THEREBY



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; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-685-239-2

Query Match          13.2%; Score 120.5; DB 3; Length 163;
Best Local Similarity 26.3%; Pred. No. 1e-05;
Matches 40; Conservative 22; Mismatches 49; Indels 41; Gaps 7;

QY 15 HTYSHPSCPSGQDTSSELLRWSTVPV-----PLEPARPNRHPESCRASEDGPLNSRA 70
    ||: | || ||| | : | : | : ||:
Db 38 HTFFQPESCP-----PYPGGSMKLDIGIN---ENQRVMSMRNIESRS 78

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QY      71  ISPWRYELDRNLKRLPODDYLHARCLCPHCVSVLSOTGSHMDPRGNSELLLYHN-----QIVFY 125
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Db      79  TSPWNTVTWDPNRYRSEVVQAOCNRNLGGCINAQ-----GREDISMNSVP IQOETLTV 130

QY      126  RRPCHEGEKTHKGCYCLERLRYSVLACVCVRP 157
Db      131  RRK---HQGCSVSFQLEKVL--VTVGCTCVTP 157

RESULT 6
US-08-432-994A-8
; Sequence 8, Application US/08432994A
; Patent No. 6274711
; GENERAL INFORMATION:
; APPLICANT: Golstein, Pierre
; APPLICANT: Rohvier, Eric

```

APPLICANT: Lebecque, Serge J.E.  
 APPLICANT: Djossou, Odile  
 APPLICANT: Banchereau, Jacques  
 TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND  
 TITLE OF INVENTION: RELATED REAGENTS  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DNAX Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/432,994A  
 FILING DATE: 02-MAY-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/250,846  
 FILING DATE: 27-MAY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/177,747  
 FILING DATE: 05-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/077,203  
 FILING DATE: 14-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0388k3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-9196  
 TELEFAX: 415-496-1200  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 155 amino acids

;  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-432-994A-8

Query Match 10.6%; Score 96.5; DB 4; Length 155;  
Best Local Similarity 25.8%; Pred. No. 0.0041;  
Matches 34; Conservative 15; Mismatches 58; Indels 25; Gaps 5;

QY 45 PLEPARPNRHPSG-----RASEDGPLNS-----RAISPWRYELDRDLNRLPQ 87

Db 28 PRNPGCPNSEDKNFPTVAVNLNIHNRNTNPKRSDYNNRSTSPWNLHRNEDPERYS 87

QY 88 DLYHARCLPHCVSLQSGSHMPDRGNSSELYLHNQTYFYRRPCHGKGTGKGYCLERLXR 147

Db 88 VIWEAK--CRHLGCINADGNDVDYHMSVPIQOEILVLRREPPH-----CPNSFRLEKIL-- 139

QY 148 VSLACVCPVRPV 159

Db 140 VSVGCTCTPIV 151

## RESULT 7

US-08-620-694A-8  
; Sequence 8, Application US/08620694A  
; Patent No. 5869286

## GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694A  
FILING DATE: 21 MARCH 1996

## CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995

## CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995

## CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)

## INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:

;  
; ORGANISM: Herpesvirus Saimiri  
; STRAIN: ORF13  
US-08-620-694A-8

Query Match 10.2%; Score 92.5; DB 2; Length 151;  
Best Local Similarity 27.7%; Pred. No. 0.011;  
Matches 31; Conservative 19; Mismatches 43; Indels 19; Gaps 5;

QY 52 NRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLPHCVSLQSGSHMDPR 111

Db 51 NWTSTSKRASD---YYNRSTSPWTLHRNEDODRYPVWEAKCRYLGCVNAD----- 99

QY 112 GNSSELYHNQTYFYRRPC-----HGEKGTGKGYCLERLRYRVSACVCPVRPV 159

Db 100 GNVD--YHMSVPIQOEILVVRKGHGPCNPSFRLEKML--VTVGCTCTPIV 147

## RESULT 8

US-09-034-810-6  
; Sequence 6, Application US/09034810  
; Patent No. 6043344

## GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth  
APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKeough  
APPLICANT: Goldman, Samuel  
APPLICANT: Pittman, Debra  
APPLICANT: Mi, Sha  
APPLICANT: Neben, Steven  
APPLICANT: Giannotti, JoAnn  
APPLICANT: Golden/Fleet, Margaret  
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,810  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,239  
FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: GI5262  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

## US-09-034-810-6

Query Match 10.2%; Score 92.5; DB 3; Length 151;  
Best Local Similarity 27.7%; Pred. No. 0.011;  
Matches 31; Conservative 19; Mismatches 43; Indels 19; Gaps 5;

QY 52 NRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLPHCVSLQSGSHMDPR 111

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RESULT 10
US-09-022-696-8
; Sequence 8, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037e1 Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORF13
; US-09-022-696-8
Query Match 10.2%; Score 92.5; DB 3; Length 151;
Best Local Similarity 27.7%; Pred. No. 0.011;
Matches 31; Conservative 19; Mismatches 43; Indels
Qy 52 NRHPESCRASDGLNSRAISPRYELDRDLNRLPQDLYHARCLCPHCVCVSLQTGS
Db 51 NWNTSSKRSAD--YYNRSTSPWTLHRNEDDQDRVPVSIWEAKRYLGCVNAD---
Qy 112 GNSellylHNQTVFYRRPC----HGEXGTHKGVCYLERLYRVSACVCYVRPV 159
Db 100 GNVD--YHMNSVPIQQEILVVRKGHGPCNPSEFLKML--VTVGCTCVTPIV.147
RESULT 11
US-08-685-239-6
Sequence 6. Application US/08685239

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Search completed: May 12, 2003, 02:02:52  
Job time : 24 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2003, 01:58:09 ; Search time 29 Seconds  
(without alignments)  
510.901 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MYQVAFAMVGMTHYSHW.....ERRLYRVSLACVCVRPRVMG 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pbp.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pbp.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pbp.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pbp.\*
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- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pbp.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pbp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	910	100.0	161	10	US-09-886-404-2
2	898	98.7	177	9	US-09-874-503-6
3	898	98.7	177	9	US-10-000-157-6
4	898	98.7	177	9	US-10-063-547-156
5	898	98.7	177	9	US-09-816-744-6
6	898	98.7	177	9	US-09-747-259-6
7	898	98.7	177	9	US-10-063-616-156
8	898	98.7	177	9	US-10-063-502-156
9	898	98.7	177	9	US-10-063-518-156
10	898	98.7	177	9	US-10-063-598-156
11	898	98.7	177	9	US-10-227-693-156
12	898	98.7	177	9	US-09-908-827-6
13	898	98.7	177	9	US-10-213-181-18
14	898	98.7	177	9	US-10-063-567-156
15	898	98.7	177	9	US-10-063-538-156
16	898	98.7	177	9	US-10-063-599-156
17	898	98.7	177	9	US-10-212-912-18
18	898	98.7	177	9	US-10-213-044-18
19	898	98.7	177	9	US-10-063-595-156

20	898	98.7	177	12	US-10-006-867-156	Sequence 156, App
21	709	77.9	169	10	US-09-886-404-4	Sequence 4, Appli
22	670	73.6	159	10	US-09-886-404-10	Sequence 10, Appl
23	170.5	18.7	206	10	US-09-854-280-24	Sequence 24, Appl
24	170.5	18.7	206	10	US-09-854-208-24	Sequence 24, Appl
25	165.5	18.2	197	9	US-09-874-503-4	Sequence 4, Appli
26	165.5	18.2	197	9	US-10-000-157-4	Sequence 4, Appli
27	165.5	18.2	197	9	US-10-036-041-11	Sequence 11, Appl
28	165.5	18.2	197	9	US-09-320-713-29	Sequence 29, Appl
29	165.5	18.2	197	9	US-09-816-744-4	Sequence 4, Appli
30	165.5	18.2	197	9	US-09-747-259-4	Sequence 4, Appli
31	165.5	18.2	197	9	US-10-035-855-11	Sequence 11, Appl
32	165.5	18.2	197	9	US-10-174-590-448	Sequence 448, App
33	165.5	18.2	197	9	US-10-176-758-448	Sequence 448, App
34	165.5	18.2	197	9	US-10-175-737-448	Sequence 448, App
35	165.5	18.2	197	9	US-10-173-706-448	Sequence 448, App
36	165.5	18.2	197	9	US-10-175-738-448	Sequence 448, App
37	165.5	18.2	197	9	US-10-175-752-448	Sequence 448, App
38	165.5	18.2	197	9	US-10-176-482-448	Sequence 448, App
39	165.5	18.2	197	9	US-10-176-757-448	Sequence 448, App
40	165.5	18.2	197	9	US-10-176-913-448	Sequence 448, App
41	165.5	18.2	197	9	US-10-180-552-448	Sequence 448, App
42	165.5	18.2	197	9	US-10-180-557-448	Sequence 448, App
43	165.5	18.2	197	9	US-09-931-836-11	Sequence 11, Appl
44	165.5	18.2	197	9	US-10-173-700-448	Sequence 448, App
45	165.5	18.2	197	9	US-10-174-572-448	Sequence 448, App

#### ALIGNMENTS

#### RESULT 1

US-09-886-404-2  
; Sequence 2, Application US/09886404  
; Patent No. US20020037524A1  
; GENERAL INFORMATION:  
; APPLICANT: Medlock, Eugene  
; APPLICANT: Yeh, Richard  
; APPLICANT: Silbiger, Scott M.  
; APPLICANT: Elliot, Gary S.  
; APPLICANT: Nguyen, Hung O.  
; APPLICANT: Jing, Shugian  
; TITLE OF INVENTION: IU-17 Like Molecules and Uses Thereof  
; FILE REFERENCE: 01017/37128B  
; CURRENT APPLICATION NUMBER: US/09/886,404  
; CURRENT FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 09/810,384  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/266,159  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/213,125  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-886-404-2

Query Match 100.0%; Score 910; DB 10; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.5e-78;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYQVAFAMVGMTHYSHWPCSCFKGDTSEELLRWSTVPVPLEPARPNRHPSRCRA 60  
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Db 1 MYQVAFAMVGMTHYSHWPCSCFKGDTSEELLRWSTVPVPLEPARPNRHPSRCRA 60  
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|||||

Qy 61 SEDGFLNSRAISPNRYELDRDLNRLPQDLYHARCLCPHCVSLSQTGSHMDPRGNSELYN 120  
|||||  
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Db 61 SEDGFLNSRAISPNRYELDRDLNRLPQDLYHARCLCPHCVSLSQTGSHMDPRGNSELYN 120  
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Qy 121 QTVFYRRPCHKEGTHKCYCLERRLYRSLACVCVRPRVMG 161

Db 121 QTFFRRPCHGEKTHKGYCLERRLYRVSACVCRPRVMG 161  
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RESULT 2

US-09-874-503-6  
; Sequence 6, Application US/09874503  
; Patent No. US20020177188A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jian  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Hymowitz, Sarah G.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Starovasanik, Melissa A.  
; APPLICANT: VanLookeren, Menno  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Yansura, Daniel  
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/874,503  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/253,646  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 60/244,072  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/242,837  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/175,481  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: US 60/191,007  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/213,807  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: US 60/172,096  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: US 60/138,387  
; PRIOR FILING DATE: 1999-06-09  
; PRIOR APPLICATION NUMBER: US 60/134,287  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: US 60/131,022  
; PRIOR FILING DATE: 1999-04-26  
; PRIOR APPLICATION NUMBER: US 60/130,232  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: US 60/113,621  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: US 60/085,579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: US 09/854,208  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: US 09/854,280  
; PRIOR FILING DATE: 2001-05-20  
; PRIOR APPLICATION NUMBER: US 09/816,744  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: US 09/747,259  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: US 09/644,848  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: US 09/380,142  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: US 09/380,138  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: US 09/311,832  
; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: US PCT/US01/06520  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: US PCT/US00/34956  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: US PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US PCT/US00/30873  
; PRIOR FILING DATE: 2000-11-10  
; PRIOR APPLICATION NUMBER: US PCT/US00/23328  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US PCT/US00/07532  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: US PCT/US00/05601  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US PCT/US00/04341  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: US PCT/US99/31274  
; PRIOR FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: US PCT/US99/10733  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: US PCT/US99/05028  
; PRIOR FILING DATE: 1999-03-08  
; NUMBER OF SEQ ID NOS: 39  
; SEQ ID NO 6  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-874-503-6  
  
Query Match 98.7%; Score 898; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 QVAFALAMVGTHTYSHWPSCCPKSGQDTSEELLRWSTVPVPPLEPARNRHPESCRASE 62  
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Db 19 QVAFALAMVGTHTYSHWPSCCPKSGQDTSEELLRWSTVPVPPLEPARNRHPESCRASE 78  
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QY 63 DGPLNSRAISPRWYELDRDLNRLPQDLYHARCLPHCVSLQTSGLSHMDPRGNSSELYHNQT 122  
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Db 79 DGPLNSRAISPRWYELDRDLNRLPQDLYHARCLPHCVSLQTSGLSHMDPRGNSSELYHNQT 138  
|||||  
QY 123 VFYRRPCHGEKTHKGYCLERRLYRVSACVCRPRVMG 161  
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Db 139 VFYRRPCHGEKTHKGYCLERRLYRVSACVCRPRVMG 177  
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RESULT 3  
US-10-000-157-6  
; Sequence 6, Application US/100000157  
; Publication No. US20020182673A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jian  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul L.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Hymowitz, Sarah  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Starovasanik, Melissa  
; APPLICANT: VanLookeren, Menno  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William  
; APPLICANT: Yansura, Daniel

;; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

;; FILE REFERENCE: P1381R1C1P4(US)

;; CURRENT APPLICATION NUMBER: US/10/000,157

;; CURRENT FILING DATE: 2001-10-30

;; PRIOR APPLICATION NUMBER: 60/085579

;; PRIOR FILING DATE: 1998-05-15

;; PRIOR APPLICATION NUMBER: 60/113621

;; PRIOR FILING DATE: 1998-12-23

;; PRIOR APPLICATION NUMBER: 60/130232

;; PRIOR FILING DATE: 1999-04-21

;; PRIOR APPLICATION NUMBER: 60/131022

;; PRIOR FILING DATE: 1999-04-26

;; PRIOR APPLICATION NUMBER: 60/134287

;; PRIOR FILING DATE: 1999-05-14

;; PRIOR APPLICATION NUMBER: 60/138387

;; PRIOR FILING DATE: 1999-06-09

;; PRIOR APPLICATION NUMBER: 60/172096

;; PRIOR FILING DATE: 1999-12-23

;; PRIOR APPLICATION NUMBER: 60/175481

;; PRIOR FILING DATE: 2000-01-11

;; PRIOR APPLICATION NUMBER: 60/191007

;; PRIOR FILING DATE: 2000-03-21

;; PRIOR APPLICATION NUMBER: 60/213807

;; PRIOR FILING DATE: 2000-06-22

;; PRIOR APPLICATION NUMBER: 60/242837

;; PRIOR FILING DATE: 2000-10-24

;; PRIOR APPLICATION NUMBER: 60/244072

;; PRIOR FILING DATE: 2000-10-26

;; PRIOR APPLICATION NUMBER: 60/253646

;; PRIOR FILING DATE: 2000-11-28

;; PRIOR APPLICATION NUMBER: 09/311832

;; PRIOR FILING DATE: 1999-05-14

;; PRIOR APPLICATION NUMBER: 09/380138

;; PRIOR FILING DATE: 1999-08-25

;; PRIOR APPLICATION NUMBER: 09/380142

;; PRIOR FILING DATE: 1999-08-25

;; PRIOR APPLICATION NUMBER: 09/644848

;; PRIOR FILING DATE: 2000-08-22

;; PRIOR APPLICATION NUMBER: 09/747259

;; PRIOR FILING DATE: 2000-12-20

;; PRIOR APPLICATION NUMBER: 09/816744

;; PRIOR FILING DATE: 2001-03-22

;; PRIOR APPLICATION NUMBER: 09/854208

;; PRIOR FILING DATE: 2001-05-10

;; PRIOR APPLICATION NUMBER: 09/854280

;; PRIOR FILING DATE: 2001-05-10

;; PRIOR APPLICATION NUMBER: 09/874503

;; PRIOR FILING DATE: 2001-06-05

;; PRIOR APPLICATION NUMBER: 09/908827

;; PRIOR FILING DATE: 2001-07-18

;; PRIOR APPLICATION NUMBER: 09/918585

;; PRIOR FILING DATE: 2001-07-30

;; PRIOR APPLICATION NUMBER: 09/929404

;; PRIOR FILING DATE: 2001-08-13

;; PRIOR APPLICATION NUMBER: 09/931836

;; PRIOR FILING DATE: 2001-08-16

;; PRIOR APPLICATION NUMBER: PCT/US99/05028

;; PRIOR FILING DATE: 1999-03-08

;; PRIOR APPLICATION NUMBER: PCT/US99/10733

;; PRIOR FILING DATE: 1999-05-14

;; PRIOR APPLICATION NUMBER: PCT/US99/31274

;; PRIOR FILING DATE: 1999-12-30

;; PRIOR APPLICATION NUMBER: PCT/US00/04341

;; PRIOR FILING DATE: 2000-02-18

;; PRIOR APPLICATION NUMBER: PCT/US00/05601

;; PRIOR FILING DATE: 2001-03-01

;; PRIOR APPLICATION NUMBER: PCT/US00/05841

;; PRIOR FILING DATE: 2000-03-02

;; PRIOR APPLICATION NUMBER: PCT/US00/07532

;; PRIOR FILING DATE: 2000-03-21

;; PRIOR APPLICATION NUMBER: PCT/US00/15264

;; PRIOR FILING DATE: 2000-06-02

;; PRIOR APPLICATION NUMBER: PCT/US00/23328

;; PRIOR FILING DATE: 2000-08-24

;; PRIOR APPLICATION NUMBER: PCT/US00/30873

;; PRIOR FILING DATE: 2000-11-10

;; PRIOR APPLICATION NUMBER: PCT/US00/32678

;; PRIOR FILING DATE: 2000-12-01

;; PRIOR APPLICATION NUMBER: PCT/US00/34956

;; PRIOR FILING DATE: 2000-12-20

;; PRIOR APPLICATION NUMBER: PCT/US01/06520

;; PRIOR FILING DATE: 2001-02-28

;; PRIOR APPLICATION NUMBER: PCT/US01/17800

;; PRIOR FILING DATE: 2001-06-01

;; PRIOR APPLICATION NUMBER: PCT/US01/19692

;; PRIOR FILING DATE: 2001-06-20

;; PRIOR APPLICATION NUMBER: PCT/US01/21066

;; PRIOR FILING DATE: 2001-06-29

;; PRIOR APPLICATION NUMBER: PCT/US01/21735

;; PRIOR FILING DATE: 2001-07-09

;; NUMBER OF SEQ ID NOS: 39

;; SEQ ID NO 6

;; LENGTH: 177

;; TYPE: PRT

;; ORGANISM: Homo Sapien

;; US-10-000-157-6

Query Match 98.7%; Score 898; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 3.8e-77;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QVAFVFLAMVGMTHYSHWPCSCPSKQDTSSELLRWSTVPPLEPARNRHPESCRASE 62

DB 19 QVAFVFLAMVGMTHYSHWPCSCPSKQDTSSELLRWSTVPPLEPARNRHPESCRASE 78

QY 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLPCHVSLQTSQSHMDPRGNSSELYHNQT 122

DB 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLPCHVSLQTSQSHMDPRGNSSELYHNQT 138

QY 123 VFYRPPCHGCKGTHKGYCLERLYRVSLACVGVPRVMG 161

DB 139 VFYRPPCHGCKGTHKGYCLERLYRVSLACVGVPRVMG 177

RESULT 4

US-10-063-547-156

;; Sequence 156, Application US/10063547

;; Publication No. US20020182638A1

;; GENERAL INFORMATION:

;; APPLICANT: Eaton, Dan L.

;; APPLICANT: Filvaroff, Ellen

;; APPLICANT: Gerritsen, Mary E.

;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.

;; APPLICANT: Grimaldi, Christopher J.

;; APPLICANT: Gurney, Austin L.

;; APPLICANT: Watanabe, Collin K.

;; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

;; TITLE OF INVENTION: ACIDS ENCODING THE SAME

;; FILE REFERENCE: P3230R1C1

;; CURRENT APPLICATION NUMBER: US/10/063,547

;; CURRENT FILING DATE: 2002-05-02

;; Prior Application removed - See File Wrapper or Palm

;; NUMBER OF SEQ ID NOS: 170

;; SEQ ID NO 156

;; LENGTH: 177

;; TYPE: PRT

;; ORGANISM: Homo Sapien

;; US-10-063-547-156

Query Match 98.7%; Score 898; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 3.8e-77;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QVAFVFLAMVGMTHYSHWPCSCPSKQDTSSELLRWSTVPPLEPARNRHPESCRASE 62

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Db 19 QVAFVAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPLEPARNRHPESCRASE 78
QY 63 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCYSLOTGSHMDPRGNSELYHNQT 122
Db 79 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCYSLOTGSHMDPRGNSELYHNQT 138
QY 123 VFYRRPCHGEGKTHKGYCLERRLYRVSLACVCRPRVMG 161
Db 139 VFYRRPCHGEGKTHKGYCLERRLYRVSLACVCRPRVMG 177

RESULT 5
US-09-816-744-6
; Sequence 6, Application US/09816744
; Publication No. US20030003546A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P2(US)
; CURRENT APPLICATION NUMBER: US/09/816,744
; PRIOR FILING DATE: 2001-03-22
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 6
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-816-744-6

Query Match 98.7%; Score 898; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8e-77;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QVAFVAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPLEPARNRHPESCRASE 62
Db 19 QVAFVAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPLEPARNRHPESCRASE 78
QY 63 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCYSLOTGSHMDPRGNSELYHNQT 122
Db 79 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCYSLOTGSHMDPRGNSELYHNQT 138
QY 123 VFYRRPCHGEGKTHKGYCLERRLYRVSLACVCRPRVMG 161
Db 139 VFYRRPCHGEGKTHKGYCLERRLYRVSLACVCRPRVMG 177

RESULT 6
US-09-747-259-6
; Sequence 6, Application US/09747259
; Publication No. US20030008815A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul

```

```

; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 6
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-747-259-6

Query Match 98.7%; Score 898; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8e-77;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QVAFVAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPLEPARNRHPESCRASE 62
Db 19 QVAFVAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPLEPARNRHPESCRASE 78
QY 63 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCYSLOTGSHMDPRGNSELYHNQT 122
Db 79 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCYSLOTGSHMDPRGNSELYHNQT 138
QY 123 VFYRRPCHGEGKTHKGYCLERRLYRVSLACVCRPRVMG 161
Db 139 VFYRRPCHGEGKTHKGYCLERRLYRVSLACVCRPRVMG 177

RESULT 7
US-10-063-616-156

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```
; Sequence 156, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 156
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-616-156

Query Match          98.7%; Score 898; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8e-77;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QVAFAMVMGTHYSHWPCSCPSKQDTSSELLRWSTVPPPLEPARNRHPESCRASE 62
Db 19 QVAFAMVMGTHYSHWPCSCPSKQDTSSELLRWSTVPPPLEPARNRHPESCRASE 78
Qy 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCPHCVSLQTSQSHMDPRGNSSELYHNQT 122
Db 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCPHCVSLQTSQSHMDPRGNSSELYHNQT 138
Qy 123 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 161
Db 139 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 177
Qy 123 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 161
Db 139 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 177

RESULT 8
US-10-063-502-156
; Sequence 156, Application US/10063502
; Publication No. US20030023042A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,502
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 156
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-502-156

Query Match          98.7%; Score 898; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8e-77;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 3 QVAFAMVMGTHYSHWPCSCPSKQDTSSELLRWSTVPPPLEPARNRHPESCRASE 62
Db 19 QVAFAMVMGTHYSHWPCSCPSKQDTSSELLRWSTVPPPLEPARNRHPESCRASE 78
Qy 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCPHCVSLQTSQSHMDPRGNSSELYHNQT 122
Db 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCPHCVSLQTSQSHMDPRGNSSELYHNQT 138
Qy 123 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 161
Db 139 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 177

RESULT 9
US-10-063-518-156
; Sequence 156, Application US/10063518
; Publication No. US20030049735A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,518
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 156
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-518-156

Query Match          98.7%; Score 898; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8e-77;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QVAFAMVMGTHYSHWPCSCPSKQDTSSELLRWSTVPPPLEPARNRHPESCRASE 62
Db 19 QVAFAMVMGTHYSHWPCSCPSKQDTSSELLRWSTVPPPLEPARNRHPESCRASE 78
Qy 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCPHCVSLQTSQSHMDPRGNSSELYHNQT 122
Db 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCPHCVSLQTSQSHMDPRGNSSELYHNQT 138
Qy 123 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 161
Db 139 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 177

RESULT 10
US-10-063-598-156
; Sequence 156, Application US/10063598
; Publication No. US20030050462A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,598
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 156
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-598-156

Query Match          98.7%; Score 898; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8e-77;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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FILE REFERENCE: P3230R1C1  
 CURRENT APPLICATION NUMBER: US/10/063.598  
 CURRENT FILING DATE: 2002-05-03  
 Prior Application removed - See File Wrapper or Palm  
 NUMBER OF SEQ ID NOS: 170  
 SEQ ID NO 156  
 LENGTH: 177  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-10-063-598-156

Query Match 98.7%; Score 898; DB 9; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QVAFAMVMTHTYSHWPCSCPKGQDTSELLRWSTVPVPPLEPARPNRHPSERASE 62  
 Db 19 QVAFAMVMTHTYSHWPCSCPKGQDTSELLRWSTVPVPPLEPARPNRHPSERASE 78  
 Qy 63 DGPLNSRAISPRWYELDRDLNRLPDLYHARCLCPHCYSLQTSQSHMDPRGNSSELYHNQT 122  
 Db 79 DGPLNSRAISPRWYELDRDLNRLPDLYHARCLCPHCYSLQTSQSHMDPRGNSSELYHNQT 138  
 Qy 123 VFYRPPCHGKGTGKGYCLERLYRVSACVCVRPRVMG 161  
 Db 139 VFYRPPCHGKGTGKGYCLERLYRVSACVCVRPRVMG 177

RESULT 11  
 US-10-227-693-156  
 Sequence 156, Application US/10227693  
 Publication No. US20030050465A1  
 GENERAL INFORMATION:  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 FILE REFERENCE: P3230R1C169  
 CURRENT APPLICATION NUMBER: US/10/227.693  
 CURRENT FILING DATE: 2002-08-26  
 PRIOR APPLICATION NUMBER: US 10/006.867  
 PRIOR FILING DATE: 2001-12-06  
 PRIOR APPLICATION NUMBER: PCT/US00/23328  
 PRIOR FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: US 09/380.137  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: PCT/US99/12252  
 PRIOR FILING DATE: 1999-06-06  
 PRIOR APPLICATION NUMBER: US 60/096.012  
 PRIOR FILING DATE: 1998-08-10  
 NUMBER OF SEQ ID NOS: 170  
 SEQ ID NO 156  
 LENGTH: 177  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-10-227-693-156

Query Match 98.7%; Score 898; DB 9; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QVAFAMVMTHTYSHWPCSCPKGQDTSELLRWSTVPVPPLEPARPNRHPSERASE 62  
 Db 19 QVAFAMVMTHTYSHWPCSCPKGQDTSELLRWSTVPVPPLEPARPNRHPSERASE 78  
 Qy 63 DGPLNSRAISPRWYELDRDLNRLPDLYHARCLCPHCYSLQTSQSHMDPRGNSSELYHNQT 122

Db 79 DGPLNSRAISPRWYELDRDLNRLPDLYHARCLCPHCYSLQTSQSHMDPRGNSSELYHNQT 138  
 Qy 123 VFYRPPCHGKGTGKGYCLERLYRVSACVCVRPRVMG 161  
 Db 139 VFYRPPCHGKGTGKGYCLERLYRVSACVCVRPRVMG 177  
 RESULT 12  
 US-09-908-827-6  
 Sequence 6, Application US/09908827  
 Publication No. US20030054442A1  
 GENERAL INFORMATION:  
 APPLICANT: Chen, Jian  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul  
 APPLICANT: Grimaldi, Christopher  
 APPLICANT: Gurney, Austin  
 APPLICANT: Li, Hanzhong  
 APPLICANT: Hillan, Kenneth  
 APPLICANT: Tumas, Daniel  
 APPLICANT: VanLookeren, Menno  
 APPLICANT: Vandlen, Richard  
 APPLICANT: Watanabe, Colin  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William  
 APPLICANT: Yansura, Daniel  
 TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
 FILE REFERENCE: P1381R1C1P1C1(US)  
 CURRENT APPLICATION NUMBER: US/09/908.827  
 CURRENT FILING DATE: 2001-07-18  
 PRIOR APPLICATION NUMBER: 60/085.579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/113.621  
 PRIOR FILING DATE: 1998-12-23  
 PRIOR APPLICATION NUMBER: 60/130.232  
 PRIOR FILING DATE: 1999-04-21  
 PRIOR APPLICATION NUMBER: 60/131.022  
 PRIOR FILING DATE: 1999-04-26  
 PRIOR APPLICATION NUMBER: 60/134.287  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: 60/138.387  
 PRIOR FILING DATE: 1999-06-09  
 PRIOR APPLICATION NUMBER: 60/172.096  
 PRIOR FILING DATE: 1999-12-23  
 PRIOR APPLICATION NUMBER: 60/175.481  
 PRIOR FILING DATE: 2000-01-11  
 PRIOR APPLICATION NUMBER: 60/191.007  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/213.807  
 PRIOR FILING DATE: 2000-06-22  
 PRIOR APPLICATION NUMBER: 60/242.837  
 PRIOR FILING DATE: 2000-10-24  
 PRIOR APPLICATION NUMBER: 60/244.072  
 PRIOR FILING DATE: 2000-10-26  
 PRIOR APPLICATION NUMBER: 09/311.832  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: 09/380.138  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 09/380.142  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 09/644.848  
 PRIOR FILING DATE: 2000-08-22  
 PRIOR APPLICATION NUMBER: 09/747.259  
 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: 09/816.744  
 PRIOR FILING DATE: 2001-03-22  
 PRIOR APPLICATION NUMBER: 09/854.208  
 PRIOR FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: 09/854.280  
 PRIOR FILING DATE: 2001-03-10



PRIOR APPLICATION NUMBER: PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/US00/05601  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 6  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-908-827-6

Query Match 98.7%; Score 898; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 QVAFAMVMGTHYSHWPCSCPKGQDTSELLRWSTVPVPPLEPARPNRHPESCRASE 62  
Db 19 QVAFAMVMGTHYSHWPCSCPKGQDTSELLRWSTVPVPPLEPARPNRHPESCRASE 78  
Qy 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCPHCYSLQTSLOTGSHMDPRGNSELYHNQT 122  
Db 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCPHCYSLQTSLOTGSHMDPRGNSELYHNQT 138  
Qy 123 VFYRPPCHGKGTGKGYCLERLRYVSLACVCVPRVMG 161  
Db 139 VFYRPPCHGKGTGKGYCLERLRYVSLACVCVPRVMG 177

RESULT 13  
US-10-213-181-18  
Sequence 18, Application US/10213181  
Publication No. US20030054484A1  
GENERAL INFORMATION:  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Hillan, Kenneth  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune  
FILE REFERENCE: P3133R1C7  
CURRENT APPLICATION NUMBER: US/10/213.181  
CURRENT FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: US 10/052,594  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: PCT/US00/30873

PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: US 60/177,118  
PRIOR FILING DATE: 2000-01-20  
NUMBER OF SEQ ID NOS: 24  
SEQ ID NO 18  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-213-181-18

Query Match 98.7%; Score 898; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 QVAFAMVMGTHYSHWPCSCPKGQDTSELLRWSTVPVPPLEPARPNRHPESCRASE 62  
Db 19 QVAFAMVMGTHYSHWPCSCPKGQDTSELLRWSTVPVPPLEPARPNRHPESCRASE 78  
Qy 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCPHCYSLQTSLOTGSHMDPRGNSELYHNQT 122  
Db 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCPHCYSLQTSLOTGSHMDPRGNSELYHNQT 138  
Qy 123 VFYRPPCHGKGTGKGYCLERLRYVSLACVCVPRVMG 161  
Db 139 VFYRPPCHGKGTGKGYCLERLRYVSLACVCVPRVMG 177

RESULT 14  
US-10-063-567-156  
Sequence 156, Application US/10063567  
Publication No. US20030069394A1  
GENERAL INFORMATION:  
APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,567  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 156  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-063-567-156

Query Match 98.7%; Score 898; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 19 QVAFAMVMGTHYSHWPCSCPKGQDTSELLRWSTVPVPPLEPARPNRHPESCRASE 78  
Qy 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCPHCYSLQTSLOTGSHMDPRGNSELYHNQT 122  
Db 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCPHCYSLQTSLOTGSHMDPRGNSELYHNQT 138  
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RESULT 15  
US-10-063-538-156

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; Sequence 156, Application US/10063538
; Publication No. US20030073208A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,538
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 156
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-538-156
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Best Local Similarity 100.0%; Pred. No. 3.8e-77;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   63 DGPLNSRAISPRWYELDRDLNRLPDLYHARCLCPHCYSLQGTGSHMDPRGNSSELYHNQT 122
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Search completed: May 12, 2003, 02:02:13  
Job time : 31 secs

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 12, 2003, 02:00:49 ; Search time 1762 Seconds  
(without alignments)  
2659.223 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MYQVAFAMVMGTHYSHW.....ERRLYRVSLACVCRPRVMG 161

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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12: gb.sy.\*  
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14: gb.vi.\*  
15: em.ba.\*  
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17: em.hum.\*  
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37: em.htg.vrt.\*  
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40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	910	100.0	504	6	AX299773 Sequence
2	910	100.0	644	6	AX253225 Sequence
3	910	100.0	644	6	AX365242 Sequence
4	904	99.3	486	9	AF458059 Homo sapi
5	898	98.7	1320	6	AX092424 Sequence
6	898	98.7	1320	6	AX164145 Sequence
7	898	98.7	1320	6	AX180768 Sequence
8	898	98.7	1335	9	AF305200 Homo sapi
9	709	77.9	985	6	AX299775 Sequence
10	709	77.9	985	10	AF458060 Mus muscu
11	709	77.9	1013	6	AX365244 Sequence
12	693	76.2	1496	6	AX365250 Sequence
13	652	71.6	462	10	AY034088 Sequence
14	495	54.4	157910	9	CNS01DTR Human chr
15	495	54.4	196292	9	CNS0000B Human chr
16	430.5	47.3	145762	2	AC130940 Rattus no
17	430.5	47.3	160950	2	AC119293 Rattus no
c 17	314.5	34.6	170032	2	AC116673 Mus muscu
c 18	277	30.4	160950	2	AC119293 Rattus no
c 20	277	30.4	171821	2	AC115371 Rattus no
21	171	18.8	585	10	AF458061 Mus muscu
22	167	18.4	591	6	AX427978 Sequence
23	167	18.4	1047	6	AX180766 Sequence
24	167	18.4	1047	6	AX376380 Sequence
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26	167	18.4	1078	9	AF142410 Homo sapi
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34	125.5	13.8	687	6	AX055448 Sequence
35	125.5	13.8	687	6	AX180764 Sequence
36	125.5	13.8	687	6	AX464312 Sequence
37	125.5	13.8	687	9	AF152098 Homo sapi
38	125.5	13.8	688	9	AF184969 Homo sapi
39	125.5	13.8	703	9	AF110385 Homo sapi
40	125.5	13.8	711	9	AF212311 Homo sapi
41	125.5	13.8	736	6	AX236262 Sequence
42	125.5	13.8	1754	6	AX180770 Sequence
43	125.5	13.8	1754	6	AX358834 Sequence
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# ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO0179288.  
ACCESSION AX299773  
VERSION AX299773.1 GI:17129294  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Hurst, S.D., Zurawski, S.M. and Rennick, D.M.  
TITLE Cytokine uses; compositions; methods  
JOURNAL Patent: WO 0179288-A 1 25-OCT-2001;  
SCHERING CORPORATION (US)  
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Qy 101 SerLeuGlnThrGlySerHisMetAspProArgGlyGlnAsnSerGluLeuTyrHisAsn 120  
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Qy 121 GlnThrValPheTyrArgProCysHisGlyGlyGlyGlyThrHisLysGlyTyrCys 140  
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AX253225 644 bp DNA linear PAT 05-OCT-2001  
LOCUS AX253225  
DEFINITION Sequence 22 from Patent WO0168705.  
ACCESSION AX253225  
VERSION AX253225.1 GI:15986362  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM  
REFERENCE 1  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 644)  
Jing, S., Medlock, E., Yeh, R., Silbiger, S.M., Elliot, S.S. and  
Nguyen, H.Q.  
TITLE IL-17 receptor like molecules and uses thereof  
JOURNAL Patent: WO 0168705-A 22 20-SEP-2001;  
Amgen Inc. (US)  
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QY 121 GlnThrValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140  
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LOCUS AX365242 644 bp DNA linear PAT 15-FEB-2002  
DEFINITION Sequence 1 from Patent WO0208285.  
ACCESSION AX365242  
VERSION AX365242.1 GI:18696995  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
AUTHORS Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S., Nguyen,H.Q. and  
Jing,S.  
TITLE IL-17 molecules and uses thereof  
JOURNAL Patent: WO 0208285-A 1 31-JAN-2002;  
Amgen, Inc. (US)  
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Best Local Similarity: 100.00% Mismatches: 0  
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DEFINITION Homo sapiens IL25 mRNA, complete cds.  
ACCESSION AF458059  
VERSION AF458059.1 GI:18034675  
KEYWORDS Homo sapiens.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
AUTHORS Fort,M.M., Cheung,J., Yen,D., Li,J., Zurawski,S.M., Lo,S.,  
Menon,S., Clifford,T., Hunte,B., Lesley,R., Muchamuel,T.,  
Hurst,S.D., Zurawski,G., Leach,M.W., Gorman,D.M. and Rennick,D.M.  
TITLE IL-25 induces IL-4, IL-5, and IL-13 and Th2-associated pathologies  
in vivo  
JOURNAL Immunity 15 (6), 985-995 (2001)  
MEDLINE 21629216  
PUBMED 11754819  
REFERENCE 2 (bases 1 to 486)  
AUTHORS Hurst,S.D., Muchamuel,T., Gorman,D.M., Gilbert,J.M., Clifford,T.,  
Kwan,S., Menon,S., Seymour,B., Jackson,C., Kung,T., Brieland,J.,  
Zurawski,S.M., Chapman,R., Zurawski,G. and Coffman,R.L.  
TITLE New IL-17 family members promote Th1 or Th2 responses in the lung:  
In vivo function of the novel cytokine IL-25  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 486)  
AUTHORS Gilbert,J.M. and Gorman,D.M.  
TITLE Direct Submission  
JOURNAL Submitted (12-DEC-2001) Genomics, DNAX Research Inc., 901  
California Ave., Palo Alto, CA 94304, USA  
FEATURES Location/Qualifiers  
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Query Match: 99.34% Indels: 0

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Qy 61 SerGluAspGlyProLeuAsnSerArgAlaIleSerProTTPArgTyrGluLeuAspArg 80
Db 181 AGTGAAGATGACCCCTCAACAGCAGGCGCCATCTCCCTGGAGATATGAGTTGGACAGA 240
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Qy 101 SerLeuGlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsn 120
Db 301 AGCCTACAGACAGGCTCCACATGACACCCCGGGGCAACTCGGAGCTGCTTACCAACAAC 360
Qy 121 GlnThrValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140
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Qy 141 LeuGluArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMet 160
Db 421 CTGAGGCGCAGGCTGACCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
RESULT 5
LOCUS AX092424 1320 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 155 from Patent WO0116318.
ACCESSION AX092424
VERSION AX092424.1 GI:13444526
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 155 08-MAR-2001;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
1..1320
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 280 a 353 c 384 g 303 t
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Alignment Scores: 7.6e-54 Length: 1320
Pred. No.: 898.00 Matches: 159
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 98.68% Gaps: 0
DB: 6
US-10-037-591A-2 (1-161) x AX092424 (1-1320)
Qy 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
Db 313 CAGGTGGTGGCATCTTGGCAATGTCATGGGAACCCACACCTACAGCCACTGGCCGAGC 372
Qy 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCTGCCCCAGCAAGGCGGACACCTCTGAGGAGCTCTGAGGTGGAGCACTGTGCTCT 432
Qy 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCCCTCCCTAGAGCCCTGCTAGGCCCAACCCACCCAGAGTCTCTAGGGCCAGTGAA 492
Qy 63 AspGlyProLeuAsnSerArgAlaIleSerProTTPArgTyrGluLeuAspArgAspLeu 82
Db 493 GATGAGCCCTCAACAGCAGGCGCCATCTCCCTTGGAGATATGAGTTGGACAGAGACTTG 552
Qy 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102
Db 553 AACCGGCTCCCCAGGACCTGTACCAAGCCCTGCTGCTGCGCGCACTGCGTCAGCCTA 612
Qy 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122
Db 613 CAGACAGGCTCCACATGAGACCCCGGGGCAACTCGGAGCTGCTTACCAACACAGACT 672
Qy 123 ValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142
Db 673 GTCTTCTACAGGCGCCATGCGATGCGGAGAGGCGCACCAAGGCTACTGCTGCTGGAG 732
Qy 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161
Db 733 CCGAGGCTGACCGCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 789
RESULT 6
LOCUS AX164145 1320 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 17 from Patent WO0140465.
ACCESSION AX164145
VERSION AX164145.1 GI:14545087
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Fong,S., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L.,
Hillan,K.J., Tumas,D., Watanabe,C.K., Wood,W.I. and Zhang,Z.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0140465-A 17 07-JUN-2001;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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BASE COUNT 280 a 353 c 384 g 303 t
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Alignment Scores: 7.6e-54 Length: 1320
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Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
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DB: 6
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Qy 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
Db 313 CAGGTGGTGGCATCTTGGCAATGTCATGGGAACCCACACCTACAGCCACTGGCCGAGC 372
Qy 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCTGCCCCAGCAAGGCGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCTCT 432
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QY 43 ValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62  
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Db 433 GTCCCTCCCTAGAGCTGCTAGGCCAACCGCCACCCAGAGTCTGTAGGCCAGTGAA 492  
QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82  
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Db 493 GATGGACCCCTCAACAGCAGGGCCCTCTCCCTCTGGAGATATGAGTTGGACAGAGACTTG 552  
QY 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102  
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Db 613 CAGACAGGCTCCCAACAGCAGGGCCCTCTCCCTCTGGAGATATGAGTTGGACAGAGACTTG 612  
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Db 673 GTCTTCTACAGGGCCCATGCCATGGCAGAGAGGACCCACAGGGCTACTGCTGAGG 732  
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Db 733 CGCAGGCTGTACGCTGTTCTTCTAGCTGTGTGTGTGGCGCCCGTGTGTGGGC 789  
RESULT 7  
AX180768  
LOCUS AX180768 1320 bp DNA linear PAT 06-AUG-2001  
DEFINITION Sequence 5 from Patent WO0146420.  
ACCESSION AX180768  
VERSION AX180768.1 GI:15132618  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Chen, J., Fillvaroff, E., Fong, S., Goddard, A., Godowski, P. J.,  
Grimaldi, C. J., Gurney, A. L., Li, H., Hillan, K. J., Tumas, D., van  
Lookeren, M., Vandlen, R. L., Watanabe, C. K., Williams, P. M., Wood, W. I.  
and Yansura, D. G.  
TITLE IL-17 and IL-17r homologous polypeptides and therapeutic uses  
thereof  
JOURNAL Patent: WO 0146420-A 5 28-JUN-2001;  
Genentech, Inc. (US)  
FEATURES  
Source  
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Location/Qualifiers  
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BASE COUNT 280 a 353 c 384 g 303 t  
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Alignment Scores:  
Pred. No.: 7.6e-54 Length: 1320  
Score: 898.00 Matches: 159  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.68% Indels: 0  
DB: 6 Gaps: 0  
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Db 313 CAGGTGGTTGCAATCTTGCAATGTCATGGGAACCCACCTACAGCCACTGGCCACG 372  
QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42  
|||||  
Db 373 TGCTGCCCCAGCAAGGGCAGCAGCCTCTGAGAGCTGCTGAGGTGGAGCACTGTGCCT 432  
QY 43 ValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62  
|||||  
Db 433 GTGCCTCCCTAGAGCTGCTAGGCCAACCGCCACCCAGAGTCTGTAGGCCAGTGAA 492

QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82  
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Db 493 GATGGACCCCTCAACAGCAGGGCCCTCTCCCTCTGGAGATATGAGTTGGACAGAGACTTG 552  
QY 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102  
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Db 553 AACCAGGCTCCCAACAGCAGGGCCCTCTCCCTCTGGAGATATGAGTTGGACAGAGACTTG 612  
QY 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122  
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QY 123 ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142  
|||||  
Db 673 GTCTTCTACAGGGCCCATGCCATGGCAGAGAGGACCCACAGGGCTACTGCTGAGG 732  
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Db 733 CGCAGGCTGTACGCTGTTCTTCTAGCTGTGTGTGTGGCGCCCGTGTGTGGGC 789  
RESULT 8  
AF305200  
LOCUS Homo sapiens interleukin 17E (IL17E) mRNA linear PRI 09-JAN-2001  
DEFINITION  
ACCESSION AF305200  
VERSION AF305200.1 GI:11878209  
KEYWORDS  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Lee, J., Ho, W.-H., Maruoka, M., Corpuz, R. T., Baldwin, D. T.,  
Foster, J. S., Goddard, A. D., Yansura, D. G., Vandlen, R. L., Wood, W. I.  
and Gurney, A. L.  
TITLE IL-17E, a novel proinflammatory ligand for the IL-17 receptor  
homolog IL-17R1  
JOURNAL J. Biol. Chem. 276 (2), 1660-1664 (2001)  
MEDLINE 21125711  
PUBMED 11058597  
REFERENCE 2 (bases 1 to 1335)  
AUTHORS Lee, J., Ho, W.-H., Maruoka, M., Corpuz, R. T., Baldwin, D., Foster, J. S.,  
Goddard, A. D., Yansura, D. G., Vandlen, R. L., Wood, W. I. and Gurney, A. L.  
TITLE Direct Submission  
JOURNAL Submitted (12-SEP-2000) Molecular Biology, Genentech, 1 DNA Way,  
South San Francisco, CA 94080, USA  
FEATURES  
Source  
1. 1335  
Location/Qualifiers  
/organism="Homo sapiens"  
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BASE COUNT 295 a 353 c 384 g 303 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 7.68e-54 Length: 1335  
Score: 898.00 Matches: 159  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0



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Dd	313	CAGGTGGTGATCATCTTCGGCAATGTCATGGGAACCCACACTCAGACCCTAGCCCCAGC	372
Qy	23	CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuAArgTrpSerThrValPro	42
Dd	373	TGCTGCCCCAGCAAGGCAGACACCTCTCAGGAGCTGCTGAGGTGGAGCACCTGTGGCT	432
Qy	43	ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu	62
Dd	433	GTGGCTCCCTTAGAGCTGCTAGGCCAACCGCCACCCAGAGTCTGTGTAGGCCAGTGAA	492
Qy	63	AspGlyProLeuAnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu	82
Dd	493	GATGGACCCCACAACAGCAGGCGCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTG	552
Qy	83	AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu	102
Dd	553	AACGGCTCCCCCAGGACCTGTACACGCCGCTGCTGTGCCCGCAGTCTGCCGTGAGCCTA	612
Qy	103	GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr	122
Dd	613	CAGACAGCTCCCATGTCAGCCCGCGGCACTCGGAGCTGCTCTACCAACACCACT	672
Qy	123	ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu	142
Dd	673	GTCTCTACAGCGCGCCATGTCATGGGAGAAGGCACCCCAAGGGCTACTGCTGGAG	732
Qy	143	ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly	161
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DEFINITION	Sequence 3 from Patent WO0179288.		
ACCESSION	AX299775		
VERSION	AX299775.1	GI:17129296	
KEYWORDS	unidentified.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1		
AUTHORS	Hurst,S.D., Zurawski,S.M. and Rennick,D.M.		
TITLE	Cytokine uses; compositions; methods		
JOURNAL	Patent: WO 0179288-A 3 25-OCT-2001;		
FEATURES	SCHERING CORPORATION (US)		
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Alignment Scores:	7.36e-41		Length: 985
Pred. No.:			

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Percent Similarity:	82.14%	Conservative:	9
Best Local Similarity:	76.79%	Mismatches:	22
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DB:	6	Gaps:	1

US-10-037-591A-2 (1-161) x AX299775 (1-985).

Qy	1	MetTyRGlValValAlaPheLeuAlaMetValMetGlyThrHisThrTy	----- 17
Db	1	ATGATACAGGCTGTTCATCTTGGCAATGATCGTGGAAACCCACACACCGTACGTTGCCGG	60
Qy	18	-----SerHisTrrProSerCysCysProSerLysGlyGlnAspThrSer	32
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Qy	33	GluGluLeuLeuArgTrrPrrSerThrValProValProLeuGluProAlaArgProAsn	52
Db	121	GAGGAGTGGCTGAAAGTGGAGCTCTGTCATCTGTGTCCCCCCAGAGGCTCTGAGCCACAC	180
Qy	53	ArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIleSer	72
Db	181	CACCAGCAGAAATCCTCGAGGGCCAGCAGGATGGCCCCCTCAACAGCAGGCGCATCTCT	240
Qy	73	ProTrrPrrGlyGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTrHisAla	92
Db	241	CCTTGGAGCTATGAGTTGGACAGGACTTGAATCGGGTCCCCCAGAGACCTGTACACAGT	300
Qy	93	ArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGly	112
Db	301	CGATGCCTGTGCCACACTCGCTCAGCCTACAGACAGGCTCCACATGACCCGCTGGGC	360
Qy	113	AsnSerGluLeuLeuTyHisAsnGlnThrValPheTyArgArgProCysHisGlyGlu	132
Db	361	AATCCGTGCCACTTTACCAACACAGACGGTCTTCTACCGGGCCATGCCATGGTGAG	420
Qy	133	LysGlyThrHisLysGlyTyCysLeuGluArgArgLeuTyArgValSerLeuAlaCys	152
Db	421	GAGGTACCCATCGCCGCTACTGCTTGGAGCGCAGGCTCTACCGAGTCTCCTT3GCTTGT	480
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RESULT 10	AF458060	985 bp	mRNA	linear	ROD 15-JAN
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DEFINITION	Mus musculus IL25 mRNA, complete cds.				
ACCESSION	AF458060				
VERSION	AF458060.1	GI:18034677			
KEYWORDS					
SOURCE	Mus musculus.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus				
AUTHORS	Port,M.M., Cheung,J., Yen,D., Li,J., Zurawski,S.M., Lo,S., Menon,S., Clifford,T., Hunte,B., Lesley,R., Muchamuel,T., Hurst,S.D., Zurawski,G., Leach,M.W., Gorman,D.M. and Rennick,D. IL-25 induces IL-4, IL-5, and IL-13 and Th2-associated pathologic in vivo				
TITLE	Immunity 15 (6), 985-995 (2001)				
JOURNAL	21629216				
MEDLINE	11754819				
PUBLISHED	2 (bases 1 to 985)				
REFERENCE	Hurst,S.D., Muchamuel,T., Gorman,D.M., Gilbert,J.M., Clifford,T., Kwan,S., Menon,S., Seymour,B., Jackson,C., Kung,T., Brieland,J., Zurawski,S.M., Chapman,R., Zurawski,G. and Coffman,R.L. New IL-17 family members promote Th1 or Th2 responses in the in vivo function of the novel cytokine IL-25				
AUTHORS	Unpublished				
TITLE	3 (bases 1 to 985)				
JOURNAL	Gilbert,J.M. and Gorman,D.M.				
REFERENCE					
AUTHORS					

TITLE Direct Submission  
JOURNAL Submitted (12-DEC-2001) Genomics, DNAX Research Inc., 901  
California Ave., Palo Alto, CA 94304, USA

FEATURES  
source Location/Qualifiers  
1. .985  
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BASE COUNT 199 a 296 c 268 g 222 t

ORIGIN

Alignment Scores:  
Pred. No.: 7,36e-41 Length: 985  
Score: 709.00 Matches: 129  
Percent Similarity: 82.14% Conservative: 9  
Best Local Similarity: 76.79% Mismatches: 22  
Query Match: 77.91% Indels: 8  
DB: 10 Gaps: 1

US-10-037-591A-2 (1-161) x AF458060 (1-985)

QY 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyr----- 17  
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QY 33 GluGluLeuLeuArgTrpSerThrValProValProLeuGluProAlaArgProAsn 52  
Db 121 GAGGAGTGGCTGAAGTGGAGCTCTGCAATCGGTGCCCCAGGAGCTCTGAGCCACACC 180

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QY 93 ArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGly 112  
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QY 113 AsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCysHisGlyGlu 132  
Db 361 AACTCGCTCCCACTTACCACACAGAGCGTCTTACCGGCGGCATGCCATGTGAG 420

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QY 153 ValCysValArgProArgValMet 160  
Db 481 GTGTGTGTCGCGCCCGGCTCATG 504

RESULT 11  
AX365244  
LOCUS AX365244 1013 bp DNA linear PAT 15-FEB-2002  
DEFINITION Sequence 3 from Patent WO0208285.  
ACCESSION AX365244  
VERSION AX365244.1 GI:18696997

KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S., Nguyen,H.O. and  
Jing,S.  
TITLE 11-17 molecules and uses thereof  
JOURNAL Patent: WO 0208285-A 3 31-JAN-2002;  
Amgen, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1. .1013  
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VCVRPRVMA"

BASE COUNT 227 a 297 c 268 g 221 t

ORIGIN

Alignment Scores:  
Pred. No.: 7,56e-41 Length: 1013  
Score: 709.00 Matches: 129  
Percent Similarity: 82.14% Conservative: 9  
Best Local Similarity: 76.79% Mismatches: 22  
Query Match: 77.91% Indels: 8  
DB: 6 Gaps: 1

US-10-037-591A-2 (1-161) x AX365244 (1-1013)

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Db 1 ATGTACAGGCTTGGCATCTTGGCAATGATCGTGGGAACCCACACCCGTCAGCTTGGCG 60

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Db 121 GAGGAGTGGCTGAAGTGGAGCTCTGCAATCGGTGCCCCAGGAGCTCTGAGCCACACC 180

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Db 181 CACACGACAGAACTCTGCAGGCGCAGAGGATGGCCCTCAACAGCAGGCACTCT 240

QY 73 ProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHisAla 92  
Db 241 CCTTGGAGCTATGATGGACAGGACTTGAATCGGTGCCCCAGGAGCTTACCAGCT 300

QY 93 ArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGly 112  
Db 301 CGATCGCTGTGCCACACTCGCTGAGCTACAGAGGCTCCACATGACCGCTGGCG 360

QY 113 AsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCysHisGlyGlu 132  
Db 361 AACTCGCTCCCACTTACCACACAGAGCGTCTTACCGGCGGCATGCCATGTGAG 420

QY 133 LysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArgValSerLeuAlaCys 152  
Db 421 GAAGGTACCCATCGCGCTACTGCTGGAGCGGAGGCTCTACCGAGCTCTCTTGGCTGT 480

QY 153 ValCysValArgProArgValMet 160  
Db 481 GTGTGTGTCGCGCCCGGCTCATG 504

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RESULT 12
AX365250
LOCUS
DEFINITION
ACCESSION
AX365250
VERSION
AX365250.1 GI:18696999
KEYWORDS
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S., Nguyen, H.Q. and
Jing, S.
TITLE
11-17 molecules and uses thereof
JOURNAL
Patent: WO 0208285-A 9 31-JAN-2002;
Angen, Inc. (US)
FEATURES
source
1..1496
/organism="Mus musculus"
/db_xref="taxon:10090"
511..>987
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD23797.1"
/db_xref="GI:18697000"
/translation="MIVGTHVSLRIQEGCSHLPSCPSKEQEPPEWKLWSSASVSP
PEPLGTHAESCRASKDGLNSRAISPMWYELDRNLNRVODLYHARCCLPHCVSLQ
TGSMDPLNSVPLVHNQTVFYRRPCHGEETHRRYCLERLYRSLACVCRPRVM"
BASE COUNT 347 a 417 c 410 g 322 t
ORIGIN
Alignment Scores:
Pred. No.: 1,41e-39 Length: 1496
Score: 693.00 Matches: 126
Percent Similarity: 81.93% Conservative: 10
Best Local Similarity: 75.90% Mismatches: 22
Query Match: 76.15% Indels: 8
DB: 6 Gaps: 1
US-10-037-591A-2 (1-161) x AX365250 (1-1496)
QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyr----- 17
Db 490 AAGCGTGTTCATCTTGGCAATGATCGTGGGAACCCACACCGTCAGCTTGGCGATCCAG 549
QY 18 -----SerHisTrpProSerCysProSerLySlyGlnAspThrSerGluGlu 34
Db 550 GAGGCGTCAGTCACCTGCGCAGCTGCTGCCCCAGCAAGAGCAAGAACCCCGGAGGAG 609
QY 35 LeuLeuArgTrpSerThrValProValProProLeuGluProAlaArgProAsnArgHis 54
Db 610 TGGCTGAAGTGGAGCTGCTGCTGCTGCCCCAGAGCTCTGAGCCACACCCACCAC 669
QY 55 ProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIleSerProTrp 74
Db 670 GCAGATCTCGCAGGCCACGACGAGGATGCGCCCTCAACAGCAGGCGCATCTCTCCTGG 729
QY 75 ArgTyrgluLeuAspArgAspLeuAsnArgLeuProGluAspLeuTyrgluAlaArgCys 94
Db 730 AGCTATGAGTTGGACAGGACTTGAATCGGTCGCCCCAGGACCTGTACCACGCTCGATGC 789
QY 95 LeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGlyAsnSer 114
Db 790 CTGTGCCACACTGCTGACGCTACAGACAGAGGCTCCACATGACCCGCTGGGCAACTCC 849
QY 115 GluLeuLeuTyrgHisAsnGlnThrValPheTyrgArgProCysHisGlyGluLysGly 134
Db 850 GTCCCACTTTACACACAGCAGCGGCTCTTACCGGCGGCCCATGCGCATGGCGAGGAGGT 909
QY 135 ThrHisLysGlyTyrcysLeuGluArgArgLeuTyrgValSerLeuAlaCysValCys 154
Db 910 ACCCATCGCCGCTACTGCTTGGAGGCGAGGCTCTACCGAGTCTCTCTTGGCTGTGTGTGT 969
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QY 155 ValArgProArgValmet 160
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Db 970 GTGCGGCCCCGGGTGATG 987
RESULT 13
AY034088
LOCUS
DEFINITION
Mus musculus interleukin 17E precursor, mRNA, partial cds.
ACCESSION
AY034088
VERSION
AY034088.1 GI:17266279
KEYWORDS
Mus musculus.
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 462)
Pan, G., French, D., Mao, W., Maruoka, M., Risser, P., Lee, J.,
Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P. and
Gurney, A.L.
TITLE
Forced expression of murine IL-17E induces growth retardation,
jaundice, a Th2-biased response, and multiorgan inflammation in
mice
JOURNAL
J. Immunol. 167 (11), 6559-6567 (2001)
MEDLINE
21571724
PUBMED
11714825
REFERENCE
2 (bases 1 to 462)
Pan, G., Mao, W., Maruoka, M., French, D., Risser, P., Lee, J.,
Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P. and
Gurney, A.L.
TITLE
Direct Submission
JOURNAL
Submitted (08-MAY-2001) Molecular Biology, Genentech, 1 DNA Way,
South San Francisco, CA 94080, USA
FEATURES
source
1..462
/organism="Mus musculus"
/db_xref="taxon:10090"
<1..462
/note="IL-17E; cytokine"
/codon_start=1
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/protein_id="AAK59816.1"
/db_xref="GI:17266280"
/translation="VSLRIQEGCSHLPSCPSKEQEPPEWKLWSSASVSPPEPLSHT
HAEFSRASKDGLNSRAISPMWYELDRNLNRVODLYHARCCLPHCVSLQTSMDP
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mat_peptide
1..459
/product="interleukin 17E"
/note="IL-17E; cytokine"
BASE COUNT 90 a 157 c 130 g 85 t
ORIGIN
Alignment Scores:
Pred. No.: 3.2e-37 Length: 462
Score: 652.00 Matches: 116
Percent Similarity: 86.01% Conservative: 7
Best Local Similarity: 81.12% Mismatches: 20
Query Match: 71.65% Indels: 0
DB: 10 Gaps: 0
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QY 18 SerHisTrpProSerCysProSerLySlyGlnAspThrSerGluLeuLeuArg 37
Db 28 AGTCACCTGCCCAGCTGCTGCCCCAGCAAGAGCAAGAACCCCGGAGGAGTGGCTGAAG 87
QY 38 TrpSerThrValProValProLeuGluProAlaArgProAsnArgHisProGluSer 57
Db 88 TGGAGCTCTGCATCTGTGTCCTCCCGCCAGAGCTCTGAGCCACACCCACGAGAAATCC 147
QY 58 CysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrglu 77
Db 148 TGCAGGGCCAGCAAGGATGCGCCCTCAACAGCAGGAGGCGCATCTCTCTTGGAGCTATGAG 207
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QY 78 LeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysPro 97
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Db 208 TTGCAGAGGACTGATCGGGTCCCGCCAGACCTGTACACACCTGATCCCTGTGCCCCA 267
|||||
QY 98 HisCysValSerLeuGlnThrGlySerHisMetAspProArgGlyAsnSerGluLeu 117
|||||
Db 268 CACTGGCTAGCTACAGACAGCTCCACATGACCGCTGGCAACTCCGTCCTCCACTT 327
|||||
QY 118 TyrHisAsnGlnThrValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLys 137
|||||
Db 328 TACCACACAGACAGCTCTCTACCGCGCGCCATGTCATGGTGAGGAAGTACCCATCGC 387
|||||
QY 138 GlyTyrCysLeuGluArgGLeuTyrArgValSerLeuAlaCysValCysValArgPro 157
|||||
Db 388 CACTACTGCTGGAGCGCAGCTCTACCGAGTCTCTTGGCTGTGTGTGTGTGGGCCC 447
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QY 158 ArgValMet 160
|||||
Db 448 CGGGTCATG 456
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RESULT 14
CNS01DTR 157910 bp DNA linear PRI 28-APR-2001
LOCUS Human chromosome 14 DNA sequence BAC C-2201G16 of library Caltech-D
DEFINITION from chromosome 14 of Homo sapiens (human), complete sequence.
ACCESSION AL132855
VERSION AL132855.4 GI:13897280
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 157910)
AUTHORS Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
Gyapay,G., Saurin,W. and Weissbach,J.
Sequencing of the human chromosome 14
Unpublished
2 (bases 1 to 157910)
Genoscope.
Direct Submission
Submitted (26-APR-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Apr 30, 2001 this sequence version replaced gi:12001727.
----- Genome Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
-----
The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-124D2
Downstream BAC (overlapping the SP6 end) : R-66N24 (AC-AL135999)
----- Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 6.97x in Q20 bases; sum-of-contigs
-----
Overall quality chart :
Range : bases
0 : 26
1 - 9 : 8
10 - 19 : 58
20 - 29 : 115
30 - 39 : 574
40 - 49 : 4774
50 - 59 : 7043
60 - 69 : 9171
70 - 79 : 24066
80 - 89 : 56139
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90 - 99 : 55936
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Percentage of bases with a quality value >= 40 : 99 %
Location/Qualifiers
1. 157910
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/clone="C-2201G16"
/clone_lib="Caltech-D"
13550..13694
/note="matching EMBL:AA452257
RHdb:RH92419
dbSTS:STS65422
Identified using the e-PCR software (G. Schuler)"
46758..46857
/note="matching EMBL:N91549
RHdb:RH76320
dbSTS:STS53407
Identified using the e-PCR software (G. Schuler)"
57409..57527
/note="matching EMBL:X52889
RHdb:RH96140
RHdb:RH13799
dbSTS:STS7881
Identified using the e-PCR software (G. Schuler)"
BASE COUNT 39479 a 37198 c 39593 g 41638 t 2 others
ORIGIN
Alignment Scores:
Pred. No.: 6,61e-24 Length: 157910
Score: 495,00 Matches: 158
Percent Similarity: 17,52% Conservative: 0
Best Local Similarity: 17,52% Mismatches: 1
Query Match: 54,40% Indels: 744
DB: 9 Gaps: 1
US-10-037-591A-2 (1-161) x CNS01DTR (1-157910)
QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
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Db 7164 CAGGTGGTTGCTTGGCAATGGTCATGGAAACCCACACCTACAGGCACCTGGCCAGC 7223
|||||
QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
|||||
Db 7224 TGCTGCCCCCAAGGAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCAGCTGTGCT 7283
|||||
QY 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
|||||
Db 7284 GTGCCTCCCTAGAGCTGTAGGCCCAACCCGCCACCCAGAGTCTCTGTAGGCCAGTGA 7343
|||||
QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeu----- 78
|||||
Db 7344 GATGGACCCCTCACACAGAGGCCCATCTCCCTCTGGAGATATGAGTG-AGTCTGCTGCC 7402
|||||
QY 78 ----- 78
Db 7403 CTCCCGAATGCCTGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7462
|||||
QY 78 ----- 78
Db 7463 CAGCTTACTTTCCCATTTTGTGATCTCAGAGGGGCTGTAAAGGTTTGGGAGTTAGACA 7522
|||||
QY 78 ----- 78
Db 7523 CTGTATTGAGTCTAGCTCTGACTCTCATTTGGGATGATCTTTGAGTCAATTCAAGTTTCA 7582
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QY 78 ----- 78
Db 7583 AAACCTCAGGGTTTTTTTTTTTTTTTTCACCTGCAAAATGATATAATGCCCATAGCTA 7642
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QY 78 ----- 78
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QY 160 MetGly 161  
 Db 9863 ATGGGC 9868

## RESULT 15

CNS00000B

LOCUS

DEFINITION

CNS00000B 196292 bp DNA linear PRI 22-MAY-2001

Human chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11

from chromosome 14 of Homo sapiens (Human), complete sequence.

ACCESSION

AL049829

VERSION

AL049829.4

KEYWORDS

HTG.

SOURCE

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

TITLE

JOURNAL

REFERENCE

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JOURNAL

COMMENT

TITLE

JOURNAL

REFERENCE

AUTHORS

196292 bp DNA linear PRI 22-MAY-2001  
 Human chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11  
 from chromosome 14 of Homo sapiens (Human), complete sequence.  
 AL049829  
 AL049829.4 GI:8217859  
 HTG.  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 196292)  
 Heilig, R., Petit, J. L., Vilco, V., Dasilva, C., Robert, C., Wincker, P.,  
 Brothier, P., Catolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,  
 Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C.,  
 Gyapay, G., Saurin, W. and Weissensbach, J.  
 Sequencing of the human chromosome 14.  
 Unpublished  
 2 (bases 1 to 196292)  
 Genoscope.  
 Direct Submission  
 Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 On Jun 3, 2000 this sequence version replaced gi:6138746.  
 -----  
 Genome Center  
 Center: Genoscope / Centre National de Sequencage  
 Center code: GS  
 Web site: http://www.genoscope.cns.fr/  
 Contact: Seqref@genoscope.cns.fr  
 -----  
 The following BAC sequence is oriented from the T7 to the SP6 end.  
 Upstream BAC (overlapping the T7 end) : R-244E17  
 Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC-AL132855)  
 -----  
 Summary Statistics  
 Assembly program: Phrap; version 2.0  
 Quality coverage: 7.94x in Q20 bases; sum-of-contigs  
 -----  
 Overall quality chart :  
 Range : Bases  
 0 :  
 1 - 9 :  
 10 - 19 :  
 20 - 29 : 10  
 30 - 39 : 30  
 40 - 49 : 829  
 50 - 59 : 1909  
 60 - 69 : 5193  
 70 - 79 : 18093  
 80 - 89 : 58972  
 90 - 99 : 111256  
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 Percentage of bases with a quality value >= 40 : 99 %  
 Location/Qualifiers  
 1. 196292  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="14"  
 /clone="R-124D2"  
 /clone\_lib="RPCI-11"  
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 /note="matching EMBL:AA908790  
 RHdb:RH102162  
 dbSTS:STS69699  
 Identified using the e-PCR software (G. Schuler)"  
 80433..80566  
 /note="matching EMBL:AA167748  
 STS  
 BASE COUNT 50870 a 45673 c 47123 g 52626 t  
 ORIGIN  
 Alignment Scores:

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 dbSTS:STS55514  
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 9380..93808  
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 RHdb:RH75103  
 dbSTS:STS2191  
 Identified using the e-PCR software (G. Schuler)"  
 107758..107951  
 /note="matching EMBL:R94929  
 RHdb:RH65111  
 dbSTS:STS45044  
 Identified using the e-PCR software (G. Schuler)"  
 107996..108181  
 /note="matching EMBL:D11677  
 RHdb:RH47139  
 dbSTS:STS40201  
 Identified using the e-PCR software (G. Schuler)"  
 128387..128525  
 /note="matching EMBL:H22648  
 RHdb:RH53520  
 dbSTS:STS25817  
 Identified using the e-PCR software (G. Schuler)"  
 128419..128543  
 /note="matching EMBL:R87257  
 RHdb:RH53698  
 dbSTS:STS18321  
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 138462..138738  
 /note="matching EMBL:R59134  
 RHdb:RH53972  
 dbSTS:STS2930  
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 RHdb:RH95543  
 RHdb:RH1243  
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 138568..138677  
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 RHdb:RH28671  
 dbSTS:STS20163  
 Identified using the e-PCR software (G. Schuler)"  
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 RHdb:RH28416  
 dbSTS:STS20162  
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 138805..138926  
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 RHdb:RH68657  
 dbSTS:STS48564  
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 /note="matching EMBL:AA452257  
 RHdb:RH92419  
 dbSTS:STS65422  
 Identified using the e-PCR software (G. Schuler)"  
 194804..194903  
 /note="matching EMBL:N91549  
 RHdb:RH76320  
 dbSTS:STS3407  
 Identified using the e-PCR software (G. Schuler)"







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1	121	13.3	1258	4	US-09-724-864-2	Sequence 2, Appli
2	120.5	13.2	813	1	US-08-514-014-11	Sequence 11, Appl
3	120.5	13.2	813	2	US-08-833-823-11	Sequence 11, Appl
4	120.5	13.2	813	3	US-09-034-810-1	Sequence 1, Appl
5	120.5	13.2	813	3	US-08-685-239-1	Sequence 1, Appl
6	96.5	10.6	510	4	US-08-432-994A-7	Sequence 7, Appl
7	93.5	10.3	2285	1	US-08-477-674-9	Sequence 9, Appl
8	93.5	10.3	2285	1	US-08-473-791-9	Sequence 9, Appl
9	93.5	10.3	2285	2	US-08-316-714-9	Sequence 9, Appl
10	93.5	10.3	2285	3	US-08-473-673-9	Sequence 9, Appl
11	93	10.2	2686	4	US-09-795-691-1	Sequence 1, Appl
12	92.5	10.2	456	4	US-08-432-994A-3	Sequence 3, Appl

QY	38	-----TrpSerThrValProValProProLeuGluProAlaArg	50
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QY	51	ProAsnArgHisProGluSerCysArgAlaSerGlu-----AspGlyProLeuAsn	67
Db	315	AATGCCAGTGGCCCGCGGGCGAGCGGGCGCGCGCGCGCTTCGGGCCACCCACCAAC	374
QY	68	SerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGln	87
Db	375	CTCGCGCGGTGTCGCCCTGGCGGTACAGGATTTCCTACGACCTGCTCGCTTCGCGG	434
QY	88	AspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHis	107
Db	435	TACCTCGCGAAGCTACTGCTGTGCCGAGGTGCTG-----ACCGGCTCTAC	485
QY	108	MetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPhe-----	124
Db	486	-----GGGAGGAGGACTTCCGCTTTCGAGCAGCACCCGCTCTCTCTCCAGCC	533
QY	125	-----TyrArgArg-----ProCysHisGlyGlyGlyGlyThrHisLysGlyTyrCys	140
Db	534	GTGGTGCTGCGGCGCACAGCGGCTCGCGGGGGCGGCTCTGTGTACGCCGACACTAC	593
QY	141	LeuGluArgLeuTyrArgValSerLeuAlaCysValCysVal	155
Db	594	ATC-----ACCATCCGGTGGGTGCACCTGCGTG	623
	RESULT 2		
	US-08-514-014-11		
	; Sequence 11, Application US/08514014		
	; Patent No. 5707829		
	; GENERAL INFORMATION:		
	; APPLICANT: Jacobs, Kenneth		
	; APPLICANT: McCoy, John		
	; APPLICANT: Kelleher, Kerry		
	; APPLICANT: Carlin, McKeough		
	; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS		
	; TITLE OF INVENTION: ENCODED THEREBY		
	; NUMBER OF SEQUENCES: 12		
	; CORRESPONDENCE ADDRESS:		
	; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs		
	; STREET: 87 CambridgePark Drive		
	; CITY: Cambridge		
	; STATE: Massachusetts		
	; COUNTRY: USA		
	; ZIP: 02140		
	; COMPUTER READABLE FORM:		
	; MEDIUM TYPE: Floppy disk		
	; COMPUTER: IBM PC compatible		
	; OPERATING SYSTEM: PC-DOS/MS-DOS		
	; SOFTWARE: PatentIn Release #1.0, Version #1.25		
	; CURRENT APPLICATION DATA:		
	; APPLICATION NUMBER: US/08/514,014		
	; FILING DATE:		
	; CLASSIFICATION: 514		
	; ATTORNEY/AGENT INFORMATION:		
	; NAME: Brown, Scott A.		
	; REGISTRATION NUMBER: 32,724		
	; REFERENCE/DOCKET NUMBER: GI6000		
	; TELECOMMUNICATION INFORMATION:		
	; TELEPHONE: (617) 498-8224		
	; TELEFAX: (617) 876-5851		
	; INFORMATION FOR SEQ ID NO: 11:		
	; SEQUENCE CHARACTERISTICS:		
	; LENGTH: 813 base pairs		
	; TYPE: nucleic acid		
	; STRANDEDNESS: double		
	; TOPOLOGY: linear		
	; MOLECULE TYPE: cDNA		
	; HYPOTHETICAL: NO		
	; FEATURE:		
	; NAME/KEY: CDS		

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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/514,014
;; FILING DATE: 11-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brown, Scott A.
;; REGISTRATION NUMBER: 32,724
;; REFERENCE/DOCKET NUMBER: G16000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 498-8224
;; TELEFAX: (617) 876-5851
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 813 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 86..544
;;
US-08-833-823-11
Alignment Scores:
Pred. No.: 0.00192 Length: 813
Score: 120.50 Matches: 40
Percent Similarity: 40.79% Conservative: 22
Best Local Similarity: 26.32% Mismatches: 49
Query Match: 13.24% Indels: 41
DB: 2 Gaps: 7

US-10-037-591A-2 (1-161) x US-08-833-823-11 (1-813)
QY 15 HisThrTyrSerHisTrpProSerCysProSerLysGlyGlnAspThrSerGluGlu 34
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QY 35 LeuLeuArgTrpSerThrValProValPro-----ProLeuGluProAlaArg 50
|||||:|||||:|||||:
Db 200 -----CCTGTGCCAGGAGGTAGTATGAGCTTGACATGGCATC 238
QY 51 ProAsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAla 70
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Db 239 ATCAAT-----GAAACACAGCGGTTTCCATGTCAGTAACTCGAGAGCGCGTCC 289
QY 71 IleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyr 90
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Db 290 ACCTCCCTCGGAATTACACTGTGGACCCCAACCGGTACCCCTCGGAAGTTGTA 349
QY 91 HisAlaArgCysLeuSerProHisCysValSerLeuGlnThrGlySerHisMetAspPro 110
|||||:|||||:|||||:
Db 350 CAGGCCCATGTAGGAACTGGGCTGCTGCATCAATGCTCAA-----388
QY 111 ArgGlyAsnSerGluLeuLeuTyrHisAsn-----GlnThrValPheTyr 125
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Db 389 ---GGAAGAGAGACATCTCCATGAATTCGTTCCCATCCAGCAAGACCTGGTCGTC 445
QY 126 ArgArgProCysHisGlyGlnLysGlyThrHisLysGlyTyrCysLeuGluArgArgLeu 145
|||||:|||||:|||||:
Db 446 CGGAGGAAG-----CACCAAGAGCTGCTCTGTTTCTTCCAGTTGGAGAGGTGCTG 496
QY 146 TyrArgValSerLeuAlaCysValCysValArgPro 157
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Db 497 -----GTGACTGTGGTGACCTCGTCACCCCT 526

RESULT 4
US-09-034-810-1
; Sequence 1, Application US/09034810
; Patent No. 6043344
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKenough
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;; APPLICANT: Goldman, Samuel
;; APPLICANT: Pittman, Debra
;; APPLICANT: Mi, Sha
;; APPLICANT: Neben, Steven
;; APPLICANT: Giannotti, JoAnn
;; APPLICANT: Golden/Fleet, Margaret
;; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genetics Institute, Inc.
;; STREET: 87 CambridgePark Drive
;; CITY: Cambridge
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02140
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/034,810
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/685,239
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brown, Scott A.
;; REGISTRATION NUMBER: 32,724
;; REFERENCE/DOCKET NUMBER: G15262
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 498-8224
;; TELEFAX: (617) 876-5851
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 813 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 56..544
;;
US-09-034-810-1
Alignment Scores:
Pred. No.: 0.00192 Length: 813
Score: 120.50 Matches: 40
Percent Similarity: 40.79% Conservative: 22
Best Local Similarity: 26.32% Mismatches: 49
Query Match: 13.24% Indels: 41
DB: 3 Gaps: 7

US-10-037-591A-2 (1-161) x US-09-034-810-1 (1-813)
QY 15 HisThrTyrSerHisTrpProSerCysProSerLysGlyGlnAspThrSerGluGlu 34
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Db 167 CATACATTTTTCACAAAGCCTGAGAGTTGCCCG-----199
QY 35 LeuLeuArgTrpSerThrValProValPro-----ProLeuGluProAlaArg 50
|||||:|||||:|||||:
Db 200 -----CCTGTGCCAGGAGGTAGTATGAGCTTGACATGGCATC 238
QY 51 ProAsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAla 70
|||:|||||:|||||:
Db 239 ATCAAT-----GAAACACAGCGGTTTCCATGTCAGTAACTCGAGAGCGCGTCC 289
QY 71 IleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyr 90
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Db 290 ACCTCCCTCGGAATTACACTGTGGACCCCAACCGGTACCCCTCGGAAGTTGTA 349
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Qy 91 HisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspPro 110  
Db 350 CAGGCCAGCTAGGAAGCTGGCTGCATCAATGCTCAA 388  
Qy 111 ArgGlyAsnSerGluLeuLeuTyrHisAsn 125  
Db 389 --GGAAGGAGACACATCCATGATTCCTCCAGCAGAGACCTGGTCGTC 445  
Qy 126 ArgArgProCysHisGlyGluGlySerHisLysGlyTyrCysLeuGluArgArgLeu 145  
Db 446 CGGAGGAAG-----CACCAAGGCTGCTGCTTTCTTCCAGTTGGAAGAGTGCTG 496  
Qy 146 TyrArgValSerLeuAlaCysValCysValArgPro 157  
Db 497 -----GTGACTGTGGCTGCACCTGCCTCACCCCT 526  
RESULT 5  
US-08-685-239-1  
; Sequence 1, Application US/08685239  
; Patent No. 6074849  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: Kelleher, Kerry  
; APPLICANT: Carlin, McKeough  
; APPLICANT: Goldman, Samuel  
; APPLICANT: Pittman, Debra  
; APPLICANT: Mi, Sha  
; APPLICANT: Neben, Steven  
; APPLICANT: Giannotti, JoAnn  
; APPLICANT: Golden/Fleet, Margaret  
; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,239  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; REFERENCE/DOCKET NUMBER: G15262  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 813 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 56..544  
; US-08-685-239-1  
Alignment Scores:  
Pred. No.: 0.00192 Length: 813  
Score: 120.50 Matches: 40  
Percent Similarity: 40.79% Conservative: 22  
Best Local Similarity: 26.32% Mismatches: 49

Query Match: 13.24% Indels: 41  
DB: Gaps: 7  
...US-10-037-591A-2 (1-161) x US-08-685-239-1 (1-813)  
Qy 15 HisThrTyrSerHisTyrProSerCysCysProSerLysGlyGlnAspThrSerGluGlu 34  
Db 167 CATACTTTTCCAAAAGCCTGAGAGTTGCCCG-----ProLeuGluProAlaArg 50  
Qy 35 LeuLeuArgTyrSerThrValProValPro-----CCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGCATC 238  
Db 200 -----GAAACACAGCGCTTCCATGCTCAGTAACATCAGAGCCGCTCC 289  
Qy 51 ProAsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAla 70  
Db 239 ATCAAT-----GAAACACAGCGCTTCCATGCTCAGTAACATCAGAGCCGCTCC 289  
Qy 71 IleSerProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyr 90  
Db 290 ACCTCCCTCCGATTAACACTGCTACTTGGGACCCACCGGTACCCCTCGGAAGTTGTA 349  
Qy 91 HisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspPro 110  
Db 350 CAGGCCAGCTAGGAAGCTGGCTGCATCAATGCTCAA-----GlnThrValPheTyr 125  
Qy 111 ArgGlyAsnSerGluLeuLeuTyrHisAsn-----GlnThrValPheTyr 125  
Db 389 ---GGAAGGAGACACATCCATGATTCCTCCAGCAGAGACCTGGTCGTC 445  
Qy 126 ArgArgProCysHisGlyGluGlySerHisLysGlyTyrCysLeuGluArgArgLeu 145  
Db 446 CGGAGGAAG-----CACCAAGGCTGCTGCTTTCTTCCAGTTGGAAGAGTGCTG 496  
Qy 146 TyrArgValSerLeuAlaCysValCysValArgPro 157  
Db 497 -----GTGACTGTGGCTGCACCTGCCTCACCCCT 526  
RESULT 6  
US-08-432-994A-7  
; Sequence 7, Application US/08432994A  
; Patent No. 6274711  
; GENERAL INFORMATION:  
; APPLICANT: Golstein, Pierre  
; APPLICANT: Rouvler, Eric  
; APPLICANT: Fossiez, Francois  
; APPLICANT: Lebecque, Serge J.E.  
; APPLICANT: Djossou, Odile  
; APPLICANT: Banchereau, Jacques  
; TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND  
; RELATED REAGENTS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/432,994A  
; FILING DATE: 02-MAY-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/250,846  
; FILING DATE: 27-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/177,747  
; FILING DATE: 05-JAN-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/077,203  
FILING DATE: 14-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0388K3  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 510 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 43..507  
US-08-432-994A-7

Alignment Scores:  
Pred. No.: 0.269 Length: 510  
Score: 96.50 Matches: 34  
Percent Similarity: 37.12% Conservative: 15  
Best Local Similarity: 25.76% Mismatches: 58  
Query Match: 10.60% Indels: 25  
Gaps: 5

US-10-037-591A-2 (1-161) x US-08-432-994A-7 (1-510)

QY 45 ProLeuGluProAlaArgProAsnArgHisProGluSerCys-----58  
DB 124 CCACGAATCCAGGATGCCAATCTGAGGACAGAACTTCCCGGAGCTGTGATGGTC 183  
QY 59 -----ArgAlaSerGluAspGlyProLeuAsnSer-----68  
DB 184 AACCTGAACATCCATAACCGGAATACCATACCAATCCCAAGGTCCTCAGATTACTAC 243  
QY 69 ---ArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGln 87  
DB 244 AACCGATCCACCTACCTTGGGAATCTCCACCGCAATGAGGACCTGAGAGATATCCCTCT 303  
QY 88 AspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHis 107  
DB 304 GTGATCTGGGGCAAG-----TGCAGCCACTTGGGCTGCATCAACGCTGATGGGAC 357  
QY 108 MetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArg 127  
DB 358 GTGGACTACCATCACTCTGTCCCATCCAGCAAGAGATCTGGTCTCGCGAGGGAG 417  
QY 128 ProCysHisGlyGlySerGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArg 147  
DB 418 COTCCACAC-----TGCAGCCAACTCTTCCGCTGAGAGATATCTG-----459  
QY 148 ValSerLeuAlaCysValCysValArgProArgVal 159  
DB 460 GTGCTGGGGCTGCACCTGTGTCTACCCCGGATGTC 495

## RESULT 7

US-08-477-674-9/c  
Sequence 9, Application US/08477674  
Patent No. 5644035  
GENERAL INFORMATION:  
APPLICANT: Koths, Kirston E.  
APPLICANT: Halenbeck, Robert F.  
APPLICANT: Taylor, Eric W.  
APPLICANT: Wang, Alice M.  
APPLICANT: Caspitt, Clayton L.  
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Cetus Oncology Corporation  
STREET: 1400 Fifty-Third Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,674  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/316,714  
FILING DATE:  
APPLICATION NUMBER: US/07/961,404  
FILING DATE: 15-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Kenneth M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 2595.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 420-3152  
TELEFAX: (510) 658-5470  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-477-674-9

## Alignment Scores:

Pred. No.: 4.45 Length: 2285  
Score: 93.50 Matches: 44  
Percent Similarity: 30.23% Conservative: 8  
Best Local Similarity: 25.58% Mismatches: 42  
Query Match: 10.27% Indels: 78  
Gaps: 9  
DB: 1

US-10-037-591A-2 (1-161) x US-08-477-674-9 (1-2285)

QY 9 AlaMetValMetGlyThrHisThrTyrSerHis---TyrProSerCysCysProSerLy 27  
DB 799 TCCCTGACCATGGGCACACACTCAGCATCCACACTCATGTGTGACATTCGTCGCCGGCTCC 740  
QY 27 sGlyGlnAspThrSerGluGluLeuLeuArgTyrSerThrValProValProPro----45  
DB 739 T-----TCCACAGGGCTGGGCTCCAGGTG 713  
QY 46 -----LeuGluProAlaArgPro-----51  
DB 712 GCAGTCAGGATGACCGTGTGGCCACAGAGCCGAGGGCGTCTCGCCCTGCACATTACG 653  
QY 52 -----AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnse 68  
DB 652 CTGATGGACAGGTTCGACGCCCCCTGGCTGCAAGATCTGGCCAGAGGCTCCGAGA--595  
QY 68 rArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAs 88  
DB 594 -----GCTCCCTGGAGA-----583  
QY 88 pleuTyrHisAlaArgCysLeuCys-----ProHis-----98  
DB 582 -----GCTCCAGGGTGTGGGTCTCTCTGTTTCATTGTTGTCAGACACCACACGCTCT 530  
QY 99 -----CysValSerLeuGlnThrGlySerHisMetAspProArgGlyAs 113

Db 529 CTCCTGCTGCTGCTGCTCTCAGCAGCCAGCCAGGACTTCAGTCGGCCA----- 478  
Qy 113 nSerGluLeuLeuTyHisAsnGlnThrValPheTyArgProCysHisGlyGluLy 133  
Db 477 -----GTGAGGCTCGGTTCCGTCGACTGGACCTCG 446  
Qy 133 sGlyThrHisLysGlyTyCysLeuGluArg 144  
Db 445 TCCAGCATGATGGGCGCTGATCTTGCCTGCGCGAAGG 412  
RESULT 8  
US-08-473-791-9/c  
; Sequence 9, Application US/08473791  
; Patent No. 5736340  
; GENERAL INFORMATION:  
; APPLICANT: Koths, Kirston E.  
; APPLICANT: Halenbeck, Robert F.  
; APPLICANT: Taylor, Eric W.  
; APPLICANT: Wang, Alice M.  
; APPLICANT: Casipit, Clayton L.  
; TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cetus Oncology Corporation  
; STREET: 1400 Fifty-Third Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/473,791  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/316,714  
; FILING DATE:  
; APPLICATION NUMBER: US/07/961,404  
; FILING DATE: 15-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Kenneth M.  
; REGISTRATION NUMBER: 34,174  
; REFERENCE/DOCKET NUMBER: 2595.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 420-3152  
; TELEFAX: (510) 658-5470  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2285 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-473-791-9  
Alignment Scores:  
Pred. No.: 4.45 Length: 2285  
Score: 93.50 Matches: 44  
Percent Similarity: 30.23% Conservative: 8  
Best Local Similarity: 25.58% Mismatches: 42  
Query Match: 10.27% Indels: 78  
DB: 1 Gaps: 9  
US-10-037-591a-2 (1-161) x US-08-473-791-9 (1-2285)  
Qy 9 AlaMetValMetGlyThrHisThrTySer-His---TrrProSerCysCysProSerLy 27  
Db 799 TCCCTGACCATGGGCACACACTCAGCATCCACACTCATGTGTCATGCTGCGCGCTCC 740

Qy 27 sGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValProValProPro----- 45  
Db 739 T-----TCCACAGGGCCTGGGCTCCAGGTTG 713  
Qy 46 -----LeuGluProAlaArgPro----- 51  
Db 712 GCAGTCAGGATGACCGTGTGGCCACAGAGCCAGGCGTCTTCGCCCTGCACATTCACG 653  
Qy 52 -----AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSe 68  
Db 652 CTGATGGACAGTCGACGCCGCTGGCTGTCAAGATCTGGCCAAAGGCTCCGAGA-- 595  
Qy 68 rArgAlaIleSerProTrpArgTyGluLeuAspArgAspLeuAsnArgLeuProGlnAs 88  
Db 594 -----GCTCCCTGGAGA----- 583  
Qy 88 pleuTyHisAlaArgCysLeuCys-----ProHis----- 98  
Db 582 -----GGTCCAGGCTGGGTGCTCTTCAGCCAGCCAGGACTTCGAGTCGGCCA----- 478  
Qy 99 -----CysValSerLeuGlnThrGlySerHisMetAspProArgGlyAs 113  
Db 529 CTCTCGTCTGCAGTTGCTCTTCAGCCAGCCAGGACTTCGAGTCGGCCA----- 478  
Qy 113 nSerGluLeuLeuTyHisAsnGlnThrValPheTyArgArgProCysHisGlyGluLy 133  
Db 477 -----GTGAGGCTCGGTTCCGTCGACTGGACCTCG 446  
Qy 133 sGlyThrHisLysGlyTyCysLeuGluArg 144  
Db 445 TCCAGCATGATGGGCGCTGATCTTGCCTGCGCGAAGG 412  
RESULT 9  
US-08-316-714-9/c  
; Sequence 9, Application US/08316714  
; Patent No. 5965382  
; GENERAL INFORMATION:  
; APPLICANT: Koths, Kirston E.  
; APPLICANT: Halenbeck, Robert F.  
; APPLICANT: Taylor, Eric W.  
; APPLICANT: Wang, Alice M.  
; APPLICANT: Casipit, Clayton L.  
; TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cetus Oncology Corporation  
; STREET: 1400 Fifty-Third Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/316,714  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/961,404  
; FILING DATE: 15-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Kenneth M.  
; REGISTRATION NUMBER: 34,174  
; REFERENCE/DOCKET NUMBER: 2595.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 420-3152  
; TELEFAX: (510) 658-5470  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2285 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-316-714-9



SEQUENCE CHARACTERISTICS:  
LENGTH: 2285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-316-714-9

Alignment Scores:  
Pred. No.: 4.45 Length: 2285  
Score: 93.50 Matches: 44  
Percent Similarity: 30.23% Conservative: 8  
Best Local Similarity: 25.58% Mismatches: 42  
Query Match: 10.27% Indels: 78  
DB: 2 Gaps: 9

US-10-037-591A-2 (1-161) x US-08-316-714-9 (1-2285)

Qy 9 AlaMetValMetGlyThrHisThrTySer-His---TtpProSerCysCysProSerLy 27  
Db 799 TCCCTGACCATGGGCACACACTCCACATCGTGTGCATCTGTCGCCGCTCC 740  
Qy 27 sGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValProValProPro-----45  
Db 739 T-----TCCACAGGCGCTGGGCTCCAGGTTG 713  
Qy 46 -----LeuGluProAlaArgPro-----51  
Db 712 GCAGTCAGGATGACCGTGTGGCCACAGAGCCGCGCTCTCGCCCTGCACATTCACG 653  
Qy 52 -----AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSe 68  
Db 652 CTGATGGACAGTCCGACGCCGCTGGTGTCAAGATCTGCCAAGGCCCTCCGAGA--595  
Qy 68 rArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAs 88  
Db 594 -----GCTCCCTGGAGA-----583  
Qy 88 pleuTyrHisAlaArgCysLeuCys-----ProHis-----98  
Db 582 -----GGTCCAGGATGGGCTGCTGCTGTTTCATTGGTGCACACACACACGCGTCT 530  
Qy 99 -----CysValSerLeuGlnThrGlySerHisMetAspProArgGlyAs 113  
Db 529 CTCCTGCTCCACTTCTCTTCAGCCAGCCAGGACTTCAGTCGCCCA-----478  
Qy 113 nSerGluLeuTyrHisAsnGlnThrValPheTyrArgProCysHisGlyGluLy 133  
Db 477 -----GTGAGGCGCTCGGTTCCCGTGCACCTGGACCTCG 446  
Qy 133 sGlyThrHisLysGlyTyrCysLeuGluArgArg 144  
Db 445 TCCAGCATGATGGGCGCTGATCTCTTGGCCCGAAGG 412

RESULT 10  
US-08-473-673-9/c  
Sequence 9, Application US/08473673  
Patent No. 6069127  
GENERAL INFORMATION:  
APPLICANT: Koths, Kirston E.  
APPLICANT: Halenbeck, Robert F.  
APPLICANT: Taylor, Eric W.  
APPLICANT: Wang, Alice M.  
APPLICANT: Casipit, Clayton L.  
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cetus Oncology Corporation  
STREET: 1400 Fifty-Third Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/473,673  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/316,714  
FILING DATE: 29-SEP-1994  
APPLICATION NUMBER: US/07/961,404  
FILING DATE: 15-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Kenneth M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 2595.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 420-3152  
TELEFAX: (510) 658-5470  
TELEX: N/A

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-473-673-9

Alignment Scores:  
Pred. No.: 4.45 Length: 2285  
Score: 93.50 Matches: 44  
Percent Similarity: 30.23% Conservative: 8  
Best Local Similarity: 25.58% Mismatches: 42  
Query Match: 10.27% Indels: 78  
DB: 2 Gaps: 9

US-10-037-591A-2 (1-161) x US-08-473-673-9 (1-2285)

Qy 9 AlaMetValMetGlyThrHisThrTySer-His---TtpProSerCysCysProSerLy 27  
Db 799 TCCCTGACCATGGGCACACACTCCACATCGTGTGCATCTGTCGCCGCTCC 740  
Qy 27 sGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValProValProPro-----45  
Db 739 T-----TCCACAGGCGCTGGGCTCCAGGTTG 713  
Qy 46 -----LeuGluProAlaArgPro-----51  
Db 712 GCAGTCAGGATGACCGTGTGGCCACAGAGCCGCGCTCTCGCCCTGCACATTCACG 653  
Qy 52 -----AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSe 68  
Db 652 CTGATGGACAGTCCGACGCCGCTGGTGTCAAGATCTGCCAAGGCCCTCCGAGA--595  
Qy 68 rArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAs 88  
Db 594 -----GCTCCCTGGAGA-----583  
Qy 88 pleuTyrHisAlaArgCysLeuCys-----ProHis-----98  
Db 582 -----GGTCCAGGATGGGCTGCTGCTGTTTCATTGGTGCACACACACACGCGTCT 530  
Qy 99 -----CysValSerLeuGlnThrGlySerHisMetAspProArgGlyAs 113  
Db 529 CTCCTGCTCCACTTCTCTTCAGCCAGCCAGGACTTCAGTCGCCCA-----478  
Qy 113 nSerGluLeuTyrHisAsnGlnThrValPheTyrArgProCysHisGlyGluLy 133  
Db 477 -----GTGAGGCGCTCGGTTCCCGTGCACCTGGACCTCG 446

QY 133 sGlyThrHisLysGlyTyrCysLeuGluArg 144  
Db 445 TCCAGCATGATGGGCGCTGATCTTGCCTGAAG 412

## RESULT 11

US-09-795-691-1/c  
; Sequence 1, Application US/09795691  
; Patent No. 6465230  
; GENERAL INFORMATION:  
; APPLICANT: Meyers, Rachel  
; TITLE OF INVENTION: 27411, A No. 6465230el Human PCP Synthase  
; FILE REFERENCE: 35800/209284  
; CURRENT APPLICATION NUMBER: US/09/795,691  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/185,517  
; PRIOR FILING DATE: 2000-02-28  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2686  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (315)...(1985)  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(2686)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-795-691-1

Alignment Scores:  
Pred. No.: 6.27 Length: 2686  
Score: 93.00 Matches: 32  
Percent Similarity: 38.24% Conservative: 7  
Best Local Similarity: 31.37% Mismatches: 32  
Query Match: 10.22% Indels: 31  
Gaps: 4

US-10-037-591A-2 (1-161) x US-09-795-691-1 (1-2686)

QY 13 GlyThrHisThrTyrSerHisThrProSerCysPro----- 25  
Db 577 GGAACCGAGTTTCTGATCCACTGGAACCGGTCACCGCTTCTGGACACAGGCAGCAAGT 518  
QY 26 -----SerLysGlyGlnAspThrSerGlu 34  
Db 517 GGGAGGTGACCTGGGACACAGCTGGGACACAGCAAGGGACCAATACAGCATGTTGAC 458  
QY 35 LeuLeuArgTrpSerThrValProValPro-----Pro 45  
Db 457 CTCCTGCGCTGGCGTCCCGGTTCTGCGGAGCGGTCGGACAGCGCTCCAGGAGCGCG 398  
QY 46 LeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGluAspGlyPro 65  
Db 397 GCCAGCCTGGCGGCGGACGAGGAGGAGCGAGCT---CGCCTCCAGAACACGGGTGCC 341  
QY 66 LeuAsnSerArgAlaIleSer-ProTrpArgTyrGluLeuAspArgAspLeuAsnArgIle 85  
Db 340 GCCGAGCTGCGCGCGCCACCGCCATGAGAG-----CTCGCGCGGACGCGTGGTGCAGT 287  
QY 85 uPro 86  
Db 286 CCCT 283

## RESULT 12

US-08-432-994A-3  
; Sequence 3, Application US/08432994A  
; Patent No. 6274711  
; GENERAL INFORMATION:  
; APPLICANT: Golstein, Pierre  
; APPLICANT: Rouvier, Eric  
; APPLICANT: Fossiez, Francois  
; APPLICANT: Lebecque, Serge J.E.

APPLICANT: Djossou, Odile  
APPLICANT: Banchereau, Jacques  
TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND  
TITLE OF INVENTION: RELATED REAGENTS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,994A  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/250,846  
FILING DATE: 27-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/177,747  
FILING DATE: 05-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/077,203  
FILING DATE: 14-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0388K3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 456 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..453  
US-08-432-994A-3  
Alignment Scores:  
Pred. No.: 0.583 Length: 456  
Score: 92.50 Matches: 31  
Percent Similarity: 44.64% Conservative: 19  
Best Local Similarity: 27.68% Mismatches: 43  
Query Match: 10.16% Indels: 19  
Gaps: 5  
US-10-037-591A-2 (1-161) x US-08-432-994A-3 (1-456)  
QY 52 AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIle 71  
Db 151 AACTGGAATAGTCTTCTAAAGGGCTTCAGAC-----TACTACATAGATCTACG 201  
QY 72 SerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHis 91  
Db 202 TCTCTGGACTCTCCATCGCAATGAAGATCAAGATAGATATCCCTCTGTGATTGGAA 261  
QY 92 AlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArg 111  
Db 262 GCAAAGTGTGCTACTTAGGATGTGTTAATGCTGAT----- 297  
QY 112 GlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCys----- 129

Db 298 GCGAATGTAGAC-----TACCACATGAACTCAGTCCCTATCCAAACAAGAGATTCTTAGTG 351  
QY 130 -----HisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArg 147  
Db 352 GTGCGCAAGGGCACAACCCCTGCTTATTTAGCTAGAGAGATGCTA----- 405  
QY 148 ValSerLeuAlaCysValCysValArgProArgVal 159  
Db 406 GTGAGTGTAGGCTGCACATCGCTTACTCCCATGTT 441  
RESULT 13  
US-09-034-810-5  
; Sequence 5, Application US/09034810  
; Patent No. 6043344  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: Kelleher, Kerry  
; APPLICANT: Carlin, Mckeough  
; APPLICANT: Goldman, Samuel  
; APPLICANT: Pittman, Debra  
; APPLICANT: Mi, Sha  
; APPLICANT: Neben, Steven  
; APPLICANT: Giannotti, JoAnn  
; APPLICANT: Golden/Fleet, Margaret  
; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/034,810  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/685,239  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A. 32,724  
; REGISTRATION NUMBER: G15262  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 459 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; NAME/KEY: CDS  
; LOCATION: 1..453  
US-09-034-810-5  
Alignment Scores:  
Pred. No.: 0.589  
Matches: 92.50  
Conservative: 44.64%  
Best Local Similarity: 27.68%  
Query Match: 10.16%  
DB: 3  
Length: 459  
Matches: 31  
Conservative: 19  
Mismatch: 43  
Indels: 19  
Gaps: 5

US-10-037-591A-2 (1-161) x US-09-034-810-5 (1-459)  
QY 52 AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIle 71  
Db 151 AACTGGAATACCAGTCTCTAAAGGGCTTCAGAC-----TACTACAATAGATCTACG 201  
QY 72 SerProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHis 91  
Db 202 TCTCTTGGACTCTCCATCGCATGAAGATCAAGATAGATATCCCTCTGTGATTGGAA 261  
QY 92 AlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArg 111  
Db 262 GCAAGTGTGCTACTTAGGATGTGTTAATGCTGAT----- 297  
QY 112 GlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCys----- 129  
Db 298 GGAATGTAGAC-----TACCACATGAACTCAGTCCCTATCCAAACAAGAGATTCTAGTG 351  
QY 130 -----HisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArg 147  
Db 352 GTGCGCAAGGGCACAACCCCTGCTTATTTAGGCTAGAGAGATGCTA----- 405  
QY 148 ValSerLeuAlaCysValCysValArgProArgVal 159  
Db 406 GTGAGTGTAGGCTGCACATCGCTTACTCCCATGTT 441  
RESULT 14  
US-08-685-239-5  
; Sequence 5, Application US/08685239  
; Patent No. 6074849  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: Kelleher, Kerry  
; APPLICANT: Carlin, Mckeough  
; APPLICANT: Goldman, Samuel  
; APPLICANT: Pittman, Debra  
; APPLICANT: Mi, Sha  
; APPLICANT: Neben, Steven  
; APPLICANT: Giannotti, JoAnn  
; APPLICANT: Golden/Fleet, Margaret  
; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,239  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; REFERENCE/DOCKET NUMBER: G15262  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 459 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO

FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..453  
US-08-685-239-5

Alignment Scores:  
Pred. No.: 0.589 Length: 459  
Score: 92.50 Matches: 31  
Percent Similarity: 44.64% Conservative: 19  
Best Local Similarity: 27.68% Mismatches: 43  
Query Match: 10.16% Indels: 19  
DB: 3 Gaps: 5

US-10-037-591A-2 (1-161) x US-08-685-239-5 (1-459)

Qy 52 AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIle 71  
Db 151 AACGGGAATACCGCTCTTAAGGGCTTCAGAC-----TACTACAATAGATCTACG 201  
Qy 72 SerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHis 91  
Db 202 TCTCTGGACTCCATCGCAATGAAGATCAAGATAGATATCCCTCTGTGATTGGAA 261  
Qy 92 AlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArg 111  
Db 262 GCAAAGTGTCTACTTAGGATGTGTTAATGCTGAT----- 297  
Qy 112 GlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCys----- 129  
Db 298 GGGAAATGAGAC-----TACCATGAACCTCAGTCCCTATCCACAGAGATCTAGTG 351  
Qy 130 -----HisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluAArgArgLeuTyrArg 147  
Db 352 GTGCGAAAGGCGATCAACCTGCCCTGAATTCATTAGGCTAGAGAAGATGCTA----- 405  
Qy 148 ValSerLeuAlaCysValCysValArgProArgVal 159  
Db 406 GTGACTGTAGGCTGCACATGCGTTACTCCCATTTGTT 441

RESULT 15

US-09-034-810-3

Sequence 3, Application US/09034810

Patent No. 6043344

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Mi, Sha

APPLICANT: Neben, Steven

APPLICANT: Giannotti, Johann

APPLICANT: Golden Fleet, Margaret

TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/034,810

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/685,239

FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: GI5262

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 461 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 6..455

US-09-034-810-3

Alignment Scores:

Pred. No.: 0.841 Length: 461

Score: 91.00 Matches: 36

Percent Similarity: 44.36% Conservative: 23

Best Local Similarity: 27.07% Mismatches: 52

Query Match: 10.00% Indels: 23

DB: 3 Gaps: 6

US-10-037-591A-2 (1-161) x US-09-034-810-3 (1-461)

Qy 37 ArgTrpSerThrValProValProLeuGluProAlaArgPro----- 51  
Db 58 CGGTACTCATCCCTCAAAAGTTGAGTGTCTCCAAACGGCGAGCCCAATTAATCTTCCAGA 117  
Qy 52 -----AsnArgHisProGluSerCysArgAlaSerGluAspGly 64  
Db 118 ACGTGAAGGTCAACCTGAAGTCAATCACTCCCTT-AGCTCAAAAGCGAGCTCGAGAAGG 176  
Qy 65 ProLeuAsn-----SerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82  
Db 177 CCCTCAGATTACCTCAACCGTTCACCTTCCACTCTGAGCTCTGAGCGCAATGAGGACCT 236  
Qy 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102  
Db 237 GATAGATATCCTTCTGTGATCTGGGAGGCACAGTCCCGCCACAGCGCTGTCTCAACGCT 296  
Qy 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuTyrHisAsnGlnThr 122  
Db 297 GAG-----GGGAAGTTGGACCCACCATGAATTTCTTCTCATCCAGCAAGAGATACTA 350  
Qy 123 ValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142  
Db 351 GTCCTGAGAGAGGAGCCT-----GAGAAGTCCCCCTTCACT---TTCCGGGTGGAG 398  
Qy 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysVal 155  
Db 399 AAGATGCTG-----GTGGCGTGGGCTGCACCTGCGTT 431

Search completed: May 12, 2003, 02:54:31

Job time : 47 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 12, 2003, 02:02:59 ; Search time 98 Seconds  
(without alignments)  
2041.587 Million cell updates/sec

Title: US-10-037-591A-2  
Perfect score: 910  
Sequence: 1 MYQVAFAMVGMGTHYTSW.....ERRLYRVSLACVCRVRVMG 161

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 783854 seqs, 621352466 residues

Total number of hits satisfying chosen parameters: 1567708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USP70\_spool/US10037591/runat\_06052003\_123155\_22331/app\_query.fasta\_1.327  
-DB=PublishedApplications\_NA -Qfmt=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10037591@cgn1.1.91@runat\_06052003\_123155\_22331  
-NCPU=6 -ICPU=3 -NO\_XLPXY -NO\_MMAPP -LARGQUERY -NEG\_SCORES=0 -WAIT -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PTCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PTCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	910	100.0	644	10	US-09-886-404-1
2	898	98.7	1320	9	US-09-874-503-5
3	898	98.7	1320	9	US-10-000-157-5
4	898	98.7	1320	9	US-10-063-547-155

5	898	98.7	1320	9	US-09-747-259-5
6	898	98.7	1320	9	US-10-063-616-155
7	898	98.7	1320	9	US-10-063-502-155
8	898	98.7	1320	9	US-10-063-518-155
9	898	98.7	1320	9	US-10-063-598-155
10	898	98.7	1320	9	US-10-227-693-155
11	898	98.7	1320	9	US-09-908-827-5
12	898	98.7	1320	9	US-10-213-181-17
13	898	98.7	1320	9	US-10-063-567-155
14	898	98.7	1320	9	US-10-063-599-155
15	898	98.7	1320	9	US-10-212-912-17
16	898	98.7	1320	9	US-10-213-044-17
17	898	98.7	1320	9	US-10-063-595-155
18	898	98.7	1320	12	US-10-006-867-155
19	709	77.9	1013	10	US-09-886-404-3
20	693	76.2	1496	10	US-09-886-404-9
21	167	18.4	594	10	US-09-854-280-17
22	167	18.4	594	10	US-09-854-208-17
23	167	18.4	1047	9	US-09-874-503-3
24	167	18.4	1047	9	US-10-000-157-3
25	167	18.4	1047	9	US-10-036-041-10
26	167	18.4	1047	9	US-09-747-259-3
27	167	18.4	1047	9	US-10-035-855-10
28	167	18.4	1047	9	US-10-174-590-447
29	167	18.4	1047	9	US-10-176-758-447
30	167	18.4	1047	9	US-10-175-737-447
31	167	18.4	1047	9	US-10-173-706-447
32	167	18.4	1047	9	US-10-175-738-447
33	167	18.4	1047	9	US-10-175-752-447
34	167	18.4	1047	9	US-10-176-482-447
35	167	18.4	1047	9	US-10-176-757-447
36	167	18.4	1047	9	US-10-176-913-447
37	167	18.4	1047	9	US-10-180-552-447
38	167	18.4	1047	9	US-10-180-557-447
39	167	18.4	1047	9	US-09-931-836-10
40	167	18.4	1047	9	US-10-173-700-447
41	167	18.4	1047	9	US-10-174-572-447
42	167	18.4	1047	9	US-10-174-579-447
43	167	18.4	1047	9	US-10-174-582-447
44	167	18.4	1047	9	US-10-174-588-447
45	167	18.4	1047	9	US-10-175-739-447

ALIGNMENTS

RESULT 1  
US-09-886-404-1  
; Sequence 1, Application US/09886404  
; Patent No. US20020037524A1  
; GENERAL INFORMATION:  
; APPLICANT: Medlock, Eugene  
; APPLICANT: Yeh, Richard  
; APPLICANT: Silbiger, Scott M.  
; APPLICANT: Elliott, Gary S.  
; APPLICANT: Nguyen, Hung Q.  
; APPLICANT: Jing, Shuqian  
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof  
; FILE REFERENCE: 01017/37128B  
; CURRENT APPLICATION NUMBER: US/09/886,404  
; CURRENT FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 09/810,384  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/266,159  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/213,125  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 644  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

**TITLE OF INVENTION:** IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

**FILE REFERENCE:** P1381R1C1P3(US)

**CURRENT APPLICATION NUMBER:** US/09/874,503

**PRIOR FILING DATE:** 2001-06-05

**PRIOR APPLICATION NUMBER:** US 60/253,646

**PRIOR FILING DATE:** 2000-11-28

**PRIOR APPLICATION NUMBER:** US 60/244,072

**PRIOR FILING DATE:** 2000-10-26

**PRIOR APPLICATION NUMBER:** US 60/242,837

**PRIOR FILING DATE:** 2000-10-24

**PRIOR APPLICATION NUMBER:** US 60/175,481

**PRIOR FILING DATE:** 2000-01-11

**PRIOR APPLICATION NUMBER:** US 60/191,007

**PRIOR FILING DATE:** 2000-03-21

**PRIOR APPLICATION NUMBER:** US 60/213,807

**PRIOR FILING DATE:** 2000-06-22

**PRIOR APPLICATION NUMBER:** US 60/172,096

**PRIOR FILING DATE:** 1999-12-23

**PRIOR APPLICATION NUMBER:** US 60/138,387

**PRIOR FILING DATE:** 1999-06-09

**PRIOR APPLICATION NUMBER:** US 60/134,287

**PRIOR FILING DATE:** 1999-05-14

**PRIOR APPLICATION NUMBER:** US 60/131,022

**PRIOR FILING DATE:** 1999-04-26

**PRIOR APPLICATION NUMBER:** US 60/130,232

**PRIOR FILING DATE:** 1999-04-21

**PRIOR APPLICATION NUMBER:** US 60/113,621

**PRIOR FILING DATE:** 1998-12-23

**PRIOR APPLICATION NUMBER:** US 60/085,579

**PRIOR FILING DATE:** 1998-05-15

**PRIOR APPLICATION NUMBER:** US 09/854,208

**PRIOR FILING DATE:** 2001-05-10

**PRIOR APPLICATION NUMBER:** US 09/854,280

**PRIOR FILING DATE:** 2001-05-20

**PRIOR APPLICATION NUMBER:** US 09/816,744

**PRIOR FILING DATE:** 2001-03-22

**PRIOR APPLICATION NUMBER:** US 09/747,259

**PRIOR FILING DATE:** 2000-12-20

**PRIOR APPLICATION NUMBER:** US 09/644,848

**PRIOR FILING DATE:** 2000-08-22

**PRIOR APPLICATION NUMBER:** US 09/380,142

**PRIOR FILING DATE:** 1999-08-25

**PRIOR APPLICATION NUMBER:** US 09/380,138

**PRIOR FILING DATE:** 1999-08-25

**PRIOR APPLICATION NUMBER:** US 09/311,832

**PRIOR FILING DATE:** 1999-05-14

**PRIOR APPLICATION NUMBER:** US PCT/US01/06520

**PRIOR FILING DATE:** 2001-02-28

**PRIOR APPLICATION NUMBER:** US PCT/US00/34956

**PRIOR FILING DATE:** 2000-12-20

**PRIOR APPLICATION NUMBER:** US PCT/US00/32678

**PRIOR FILING DATE:** 2000-12-01

**PRIOR APPLICATION NUMBER:** US PCT/US00/30873

**PRIOR FILING DATE:** 2000-11-10

**PRIOR APPLICATION NUMBER:** US PCT/US00/23328

**PRIOR FILING DATE:** 2000-08-24

**PRIOR APPLICATION NUMBER:** US PCT/US00/15264

**PRIOR FILING DATE:** 2000-06-02

**PRIOR APPLICATION NUMBER:** US PCT/US00/07532

**PRIOR FILING DATE:** 2000-03-21

**PRIOR APPLICATION NUMBER:** US PCT/US00/05841

**PRIOR FILING DATE:** 2000-03-02

**PRIOR APPLICATION NUMBER:** US PCT/US00/05601

**PRIOR FILING DATE:** 2000-03-01

**PRIOR APPLICATION NUMBER:** US PCT/US00/04341

**PRIOR FILING DATE:** 2000-02-18

**PRIOR APPLICATION NUMBER:** US PCT/US99/31274

**PRIOR FILING DATE:** 1999-12-30

**PRIOR APPLICATION NUMBER:** US PCT/US99/10733

**PRIOR FILING DATE:** 1999-05-14

**PRIOR APPLICATION NUMBER:** US PCT/US99/05028

**PRIOR FILING DATE:** 1999-03-08

**NUMBER OF SEQ IDS NOS:** 39

**Alignment Scores:**

**Pred. No.: 8,89e-94 Length: 644**

**Score: 910.00 Matches: 161**

**Percent Similarity: 100.00% Conservative: 0**

**Best Local Similarity: 100.00% Mismatches: 0**

**Query Match: 100.00% Indels: 0**

**DB: 10 Gaps: 0**

**US-10-0377-59IA-2 (1-161) x US-09-886-404-1 (1-644)**

**QY 1 MetTyrGlnValAlaLalaPheLeuLaMetValMetGlyThrHisThrTySerHISTrp 20**

**Db 159 ATGTACAGTGTTGGTCATCTTGGCAATGTCATCGGAACCACCCATCACGCACACTGG 218**

**QY 21 ProSerCysCysProSerLySGlyGlnAspThrSerGlUGluLeuArgTrpSerThr 40**

**Db 219 CCAGCTGTGCCCCCAGCAAAGGGCAGGACCATCTGTAGGAGCTGTGAGGTGGAGCACT 278**

**QY 41 ValProValProProLeuGluProAlaAraGProAsnArqHisProGluSerCysArgAla 60**

**Db 279 GTCCCTGTGCTCCCCCTAGAGCTGTGAGCCCAACCCAGAGAGCTCTGTAGGGGCC 338**

**QY 61 SerGluAspGlyProLeuAsnSerArgAlaIleSerProTrpArgTYrglUeuAsparg 80**

**Db 339 AGTGAAGATTGACCCCTCAACAGCAGGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGA 398**

**QY 81 AspleuasnarGLueuproGlnaspteurtyrhisaalargcysleucyserprohisval 100**

**Db 399 GACTTGAACCGGCTCCGCCAGGACCTGTACCAAGCCCGCTGTGCTGCCGCACACTGGCCTC 458**

**QY 101 SerLeuGlnthrGlySerHisMetaspProaragglyasnsergluleuLeutyrrhisasn 120**

**Db 459 AGCCTACAGACAGACGCTCCACATGAGAACCCCGGGGCGAACTCGAGCTGCTACTCACACAAC 518**

**QY 121 GluthrValphetrArgArgProcysHisGlyGluLYsglyThrHislysGlyTyrCys 140**

**Db 519 CAGACTGTCTTCTACCGGGGCGCCATGCCATGCGAGAAAGGCCACCAAGGGCTACTGC 578**

**QY 141 LeugluArggLeutyryragvalerLeualaCyssValCYssValaIargProhgValmet 160**

**Db 579 CTGGAGGCGAGGCTGTACCGTGTTCCTTAGCTGTGTGTGTGGCCCGCGTGTGTGATG 638**

**QY 161 Gly 161**

**Db 639 GC 641**

**RESULT 2**

**US-09-874-503-5**

**; Sequence 5, Application US/09874503**

**; Patent No. US20020177188A1**

**; GENERAL INFORMATION:**

**; APPLICANT: Chen, Jian**

**; APPLICANT: Filvaroff, Ellen**

**; APPLICANT: Fong, Sherman**

**; APPLICANT: Goddard, Audrey**

**; APPLICANT: Godowski, Paul J.**

**; APPLICANT: Grimaldi, J.Christopher**

**; APPLICANT: Gurney, Austin L.**

**; APPLICANT: Li, Hanzhong**

**; APPLICANT: Hillan, Kenneth J.**

**; APPLICANT: Hymowitz, Sarah G.**

**; APPLICANT: Tomas, Daniel**

**; APPLICANT: Starovasinik, Melissa A.**

**; APPLICANT: VanLookeren, Menno**

**; APPLICANT: Vandlen, Richard**

**; APPLICANT: Watanabe, Colin K.**

**; APPLICANT: Williams, P.Mickey**

**; APPLICANT: Wood, William I.**

**; APPLICANT: Yansura, Daniel**

```
; SEQ ID NO 5
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-874-503-5

Alignment Scores:
Pred. No.: 4.85e-92 Length: 1320
Score: 898.00 Matches: 159
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.68% Indels: 0
DB: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-09-874-503-5 (1-1320)

Qy 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
Db 313 CAGGTGGTGGTATCTTGGCAATGCTATGGGAACCCACACCTACAGCCACTGGCCAGC 372
Qy 23 CysCysProSerLysGlyClnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCTCCCCAGCAAGGAGGAGACACCTCTGAGGAGCTGCTGAGTGAGCAGCTGTGCT 432
Qy 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCTCTCCCTAGAGCCTGCTAGGCCCAACCCACCCAGAGCTCTGTAGGSCCAGTGAA 492
Qy 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82
Db 493 GATGAGCCCTCAACAGCAGGAGCCCTCTCCCTCGAGATATGAGTTGGACAGACATTG 552
Qy 83 AsnArgLeuProGlnAspLeuThrHisAlaArgCysLeuCysProHisCysValSerLeu 102
Db 553 AACCGGCTCCCCAGGAGCTGTACACCCCGCTTCCCTGTGCCCCAGCTGCTACCAAC 612
Qy 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122
Db 613 CAGACAGGCTCCCATATGAGCCCGGGGCACTCGGAGCTGCTTACCAACACAGACT 672
Qy 123 ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142
Db 673 GTCTTCTACAGCGGCCATGCCATGCCAGAGGAGGCCACCCACCAAGGCTACTGCTGG 732
Qy 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161
Db 733 GCAGGCTGTACCGGTGTTCTTCTAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 789

RESULT 3
US-10-000-157-5
; Sequence 5, Application US/10000157
; Publication No. US20020182673A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul L.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovashnik, Melissa.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P4(US)
```



APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063.547  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 155  
LENGTH: 1320  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-063-547-155

Alignment Scores:  
Pred. No.: 4.85e-92 Length: 1320  
Score: 898.00 Matches: 159  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.68% Indels: 0  
DB: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-10-063-547-155 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22  
DB 313 CAGGTGGTTCATCTTGGCAATGTCATGGGAACCCACACCTACAGCCACTGGCCAGC 372  
QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42  
DB 373 TGTGTCGCCAGCAAGGCGAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 432  
QY 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62  
DB 433 GTGCCTCCCTTAGAGCCCTGTAGGGCCCAACCCGCCAGAGTCTCTAGGGCCAGTGAA 492  
QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeu 82  
DB 493 GATGGACCCCTCAACAGCAGGCGCCATCTCCCTGGAGATATGAGTTGCACAGAGACTTG 552  
QY 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102  
DB 553 AACCGGCTCCCGCAGGACCTGTACCAAGCCCGCTGTGCTGCGCCGACCTGCGTCAGCCTA 612  
QY 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122  
DB 613 CAGACAGGCTCCACATGGACCCCGGGCAACTCGGAGCTGCTTACCACAAACAGACT 672  
QY 123 ValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142  
DB 673 GTCTTCTACAGCGCGCCATGCCATGGCAAGAGGCGACCCACCAAGGGCTACTGCTGGAG 732  
QY 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161  
DB 733 CGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTCGGCGCCCGCTGTGTATGGGC 789

RESULT 5  
US-09-747-259-5  
Sequence 5, Application US/09747259  
Publication No. US20030008815A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin

PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/21066  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 5  
LENGTH: 1320  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-000-157-5

Alignment Scores:  
Pred. No.: 4.85e-92 Length: 1320  
Score: 898.00 Matches: 159  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.68% Indels: 0  
DB: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-10-000-157-5 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22  
DB 313 CAGGTGGTTCATCTTGGCAATGTCATGGGAACCCACACCTACAGCCACTGGCCAGC 372  
QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42  
DB 373 TGTGTCGCCAGCAAGGCGAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 432  
QY 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62  
DB 433 GTGCCTCCCTTAGAGCCCTGTAGGGCCCAACCCGCCAGAGTCTCTAGGGCCAGTGAA 492  
QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeu 82  
DB 493 GATGGACCCCTCAACAGCAGGCGCCATCTCCCTGGAGATATGAGTTGCACAGAGACTTG 552  
QY 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102  
DB 553 AACCGGCTCCCGCAGGACCTGTACCAAGCCCGCTGTGCTGCGCCGACCTGCGTCAGCCTA 612  
QY 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122  
DB 613 CAGACAGGCTCCACATGGACCCCGGGCAACTCGGAGCTGCTTACCACAAACAGACT 672  
QY 123 ValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142  
DB 673 GTCTTCTACAGCGCGCCATGCCATGGCAAGAGGCGACCCACCAAGGGCTACTGCTGGAG 732  
QY 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161  
DB 733 CGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTCGGCGCCCGCTGTGTATGGGC 789

RESULT 4  
US-10-063-547-155  
Sequence 155, Application US/10063547  
Publication No. US20020182638A1  
GENERAL INFORMATION:  
APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey

```

; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Wadlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yausura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR FILING DATE: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 5
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-747-259-5

Alignment Scores:
Pred. No.: 4,85e-92 Length: 1320
Score: 898.00 Matches: 159
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.68% Indels: 0
DB: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-09-747-259-5 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
Db 313 CAGGTGGTTGCATTCTTGGCAATGGTCAATGGGAACCCACACCTACAGCCACTGGCCAGC 372
QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCCTGCCCAAGGCGAGCAGACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 432
QY 43 ValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCCTCCCTAGAGCTGCTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGA 492
QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeu 82
Db 493 GTGACCCCTCAACAGCAGGGCCATCTCCCTTGGAGATATGAGTTGGACAGACTTG 552

; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 155
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-155

Alignment Scores:
Pred. No.: 4,85e-92 Length: 1320
Score: 898.00 Matches: 159
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.68% Indels: 0
DB: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-10-063-616-155 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
Db 313 CAGGTGGTTGCATTCTTGGCAATGGTCAATGGGAACCCACACCTACAGCCACTGGCCAGC 372
QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCCTGCCCAAGGCGAGCAGACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 432
QY 43 ValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCCTCCCTAGAGCTGCTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGA 492
QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeu 82
Db 493 GTGACCCCTCAACAGCAGGGCCATCTCCCTTGGAGATATGAGTTGGACAGACTTG 552

; Sequence 155, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 155
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-155

RESULT 6
US-10-063-616-155
; Sequence 155, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 155
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-155

QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeu 82
Db 493 GATGGACCCCTCAACAGCAGGGCCATCTCCCTTGGAGATATGAGTTGGACAGACTTG 552
QY 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102
Db 553 AACCGGCTCCCAAGGCGAGCAGTGTACACAGCCCGCTTGCCTGTGCGCCGCACTGGCTCAGCCTA 612
QY 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122
Db 613 CAGCAGAGGCTCCACATGGACCCCGGGGCAACTCGGAGCTGCTCTACCAACACAGACT 672
QY 123 ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142
Db 673 GTCTTCTACAGCGCGCCATGCCATGGCGAGAAGGGCACCCACCAAGGGCTACTGTGCTGGAG 732
QY 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161
Db 733 CGCAGGCTGTACCGCTGTTCTTAGCTTGTGTGTGCGGGCCCGCTGTGATGGGC 789

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 155
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-155

Alignment Scores:
Pred. No.: 4,85e-92 Length: 1320
Score: 898.00 Matches: 159
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.68% Indels: 0
DB: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-10-063-616-155 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
Db 313 CAGGTGGTTGCATTCTTGGCAATGGTCAATGGGAACCCACACCTACAGCCACTGGCCAGC 372
QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCCTGCCCAAGGCGAGCAGACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 432
QY 43 ValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCCTCCCTAGAGCTGCTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGA 492
QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeu 82
Db 493 GTGACCCCTCAACAGCAGGGCCATCTCCCTTGGAGATATGAGTTGGACAGACTTG 552
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Qy	123	valPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu	142
Db	673	GTCTTCACAGGGCGCCATGCCATGCGAGAAGGGCACCCACAAGGCCTACTGCTCTGGAG	732
Qy	143	ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly	161
Db	733	CGAGGCTGACCGTGTTCTTAGTCTGTGTGTGTGCGGCCCGCTGTGAAGGC	789

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RESULT 9
US-10-063-598-155
; Sequence 155, Application US/10063598
; Publication No. US20030050462A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,598
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 155
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-598-155

```

Alignment Scores:	4.85e-92	Length:	1320.
Pred. No.:	898.00	Matches:	159
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	98.68%	Gaps:	0
DB:	9		

US-10-037-591A-2 (1-161) x US-10-063-598-155 (1-1320)

Qy 3 GlnValValAlaPheLeuAlaMetValMetClyThrHisThrTyrSerHisTrpProSer 22  
 |||||  
 Db 313 CAGGTGGTTGCATTCCTGGCAATGGTCATGGGAACCCACACTACAGCCACTGSCCCAGC 372

QY 23 CysCysProSerLysGlyGlnAspThrSerCgluLeuLeuArgTrpSerThrValpro 42

DD 3/3 TGCTGCCCCAGCAGAGGGCAGGACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCGCT 432

Db 433 GTGCCTCCCTAGAGCTGCTAGGCCCAACGGCCACCCAGAGTCTGTAGGCCCAGTGAA 492

QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTyrGluLeuAspArgAspLeu 82

22	499	GN100RACCCCTCATACACACAGGCGCATCTCC	103	ASpArgLeuProGlnAspLeuTyrHisAlaIaArgCysLeu	103
23				CysProHisCysValSerLeu	104
24					105

Db 553 AACCGGCTCCCCAGGACCTGTACACGCCCGTTGCGTGTGCCCGCAC TGGT CAGCCTA 612

QY 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122

QY 123 ValPheTyrArgArgProCysHisGlyGluLuGlyThrHisLysGlyTyrCysLeuGlu 142

db 673 GTCTTCTACAGCGGCATGCCATGGCGAGAAGGGACCCACAAGGGCTACTGCCTGGAG 732

**QY**    143   ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValmetGly   161  
         |||||  
**Dd**     733   CGCAGCGTGACCGGTGTTTCCTTAGCTGTGTGTGTGGGCCCCCGTGTGATGGGC   789

RESULT 10

US-10-227-693-155

; Sequence 155, Application US/10227693

; Publication No. US20030050463A1

; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEI

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3230R1C169

; CURRENT APPLICATION NUMBER: US/10/227,693

; CURRENT FILING DATE: 2002-08-26

; PRIOR APPLICATION NUMBER: US 10/006,867

; PRIOR FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: PCT/US00/23328

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 09/380,137

; PRIOR FILING DATE: 1999-08-25

; PRIOR APPLICATION NUMBER: PCT/US99/12252

; PRIOR FILING DATE: 1999-06-06

; PRIOR APPLICATION NUMBER: US 60/096,012

; PRIOR FILING DATE: 1998-08-10

; NUMBER OF SEQ ID NOS: 170

```

; SEQ ID NO 155
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-227-693-155

Alignment Scores:
Pred. No.: 4.85e-92
Score: 898.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 98.68%
DB: 9
Length: 1320
Matches: 159
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

```

US-10-037-591A-2 (1-161) x US-10-227-693-155 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22

313 CAGGTGGTTGCATTCTTTGGCAATGGTTCATGGGAACCCACACCTACAGCCACTGGCCCCAGC 378

Db 373 TGCTGCCCCAGCAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 432

Qy 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62

DD	63	AsnGlyIvProIleuAsnSerArgAlaIleLeuSerProTrnArgTrnGlnLeuAsArgAsnLeu	83
DD	435	GTCCTCTCTCTCTAGAGCCCTGCTAGGGCCCCAACCGGCCACCCAGASTCTCTGTAGGGGGCCCCAGTGA	499

Db  
493 GATGGACCCCTCAACAGCAGGGGCCAATCCCCCTGGAGATGAGTTGGACAGAGACTTG 552

Qy 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102

Qv 103 GlnThrGlySerHisMetAspProArgGluValAsnSerGluLeuLeuTyrHisAsnSerIleThr 1222

\_\_\_\_\_

Db	613	CAGAGGCTCCACATGGAGACCCCGGGGCACTCGGAGCTGCTACCAACACAGACT	671
QY	123	ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu	142
Db	673	GTCTTCTACAGCGCGCATCCATGCGGAGAGCGCACCCACAAAGGCTACTGCCTGGAG	732
QY	143	ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly	161
Db	733	CGCAGGCTGTACCGTGTTCTTCTAGCTGTGTGTGTCGGCCCGCTGTGATGGGC	789

RESULT 11

US-09-908-827-5

Sequence 5, Application US/09908827

Publication No. US20030054442A1

GENERAL INFORMATION:

APPLICANT: Chen, Jian

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

APPLICANT: Li, Hanzhong

APPLICANT: Hillan, Kenneth

APPLICANT: Tumas, Daniel

APPLICANT: VanLookeren, Menno

APPLICANT: Vandlen, Richard

APPLICANT: Watanabe, Colin

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William

APPLICANT: Yansura, Daniel

TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES

FILE REFERENCE: P1381R1C1P1C1(US)

CURRENT APPLICATION NUMBER: US/09/908,827

CURRENT FILING DATE: 2001-07-18

PRIOR APPLICATION NUMBER: 60/085,579

PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/113,621

PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: 60/130,232

PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: 60/131,022

PRIOR FILING DATE: 1999-04-26

PRIOR APPLICATION NUMBER: 60/134,287

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 60/138,387

PRIOR FILING DATE: 1999-06-09

PRIOR APPLICATION NUMBER: 60/172,096

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/175,481

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: 60/191,007

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/213,807

PRIOR FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: 60/242,837

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: 60/244,072

PRIOR FILING DATE: 2000-10-26

PRIOR APPLICATION NUMBER: 09/311,832

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 09/380,138

PRIOR FILING DATE: 1999-08-25

PRIOR APPLICATION NUMBER: 09/380,142

PRIOR FILING DATE: 1999-08-25

PRIOR APPLICATION NUMBER: 09/644,848

PRIOR FILING DATE: 2000-08-22

PRIOR APPLICATION NUMBER: 09/747,259

PRIOR FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: 09/816,744

PRIOR FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: 09/854,208

PRIOR FILING DATE: 2001-05-10







Search completed: May 12, 2003, 02:56:26  
Job time : 102 secs

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GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 12, 2003, 02:01:34 ; Search time 1059 Seconds  
(without alignments)  
2462.203 Million cell updates/sec

Title: US-10-037-591A-2  
Perfect score: 910  
Sequence: 1 MYQVAFAMVMGTHYTSW.....ERRLYRSLACVCRPRVMG 161

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DEV=xlh  
-Q/cgn2\_1/USPTO\_spool/US10037591/runat\_06052003\_123154\_22289/app\_query.fasta\_1.327  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estom:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_man:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	594	65.3	524	9	AI430337	AI430337 mf68b10.y
2	493	54.2	420	14	W88186	W88186 mf68b10.r1
3	345	37.9	344	12	BG609875	BG609875 324181.MA
4	337	37.0	553	13	BM540145	BM540145 hb18f07.g
5	139	15.3	549	14	BQ554452	BQ554452 H4028C03-
6	126.5	13.9	432	10	BE108127	BE108127 UI-R-CA0-
7	126.5	13.9	511	12	BF409208	BF409208 UI-R-BT1-
8	126.5	13.9	533	14	BQ211497	BQ211497 UI-R-DY1-
9	126.5	13.9	561	14	BQ209760	BQ209760 UI-R-DZ1-
10	126	13.8	678	14	BQ604493	BQ604493 MI-P-CP1-
11	125.5	13.8	373	9	AI867949	AI867949 wb90b08.x
12	125.5	13.8	405	9	AI375735	AI375735 ta64c02.x
13	125.5	13.8	467	9	AI370793	AI370793 ta58a04.x
14	125.5	13.8	468	9	AA780147	AA780147 af37c02.s
15	125.5	13.8	568	14	BQ574994	BQ574994 UI-H-E21-
16	125.5	13.8	629	14	BM826445	BM826445 K-EST0098
17	125.5	13.8	647	12	BF476508	BF476508 naa27b03
18	124.5	13.7	870	13	BI413156	BI413156 602990024
19	123.5	13.6	504	9	AI645992	AI645992 vw53h08.x
20	123.5	13.6	749	11	AK003506	AK003506 Mus muscu
21	120.5	13.2	502	12	BF408277	BF408277 UI-R-BJ2-
22	119.5	13.1	717	13	BI408737	BI408737 602964519
23	119	13.1	441	9	AI275406	AI275406 ql63c10.x
24	116.5	12.8	579	9	AA763404	AA763404 vw53h08.r
25	115.5	12.7	590	12	BF510968	BF510968 UI-H-B14-
26	115	12.6	396	9	AA680405	AA680405 z138h02.s
27	114.5	12.6	369	13	BI274883	BI274883 UI-R-CW0-
28	112.5	12.4	366	9	AA960023	AA960023 vw53h08.s
29	110.5	12.1	718	13	BI561289	BI561289 603256441
30	110.5	12.1	836	13	BI828970	BI828970 603074846
31	109	12.0	633	12	BF682066	BF682066 602117154
32	108	11.9	437	14	W89980	W89980 mf39h11.r1
33	108	11.9	488	14	W87101	W87101 mf38e01.r1
34	108	11.9	497	9	AA044549	AA044549 mj12c03.r
35	108	11.9	499	14	W83241	W83241 mf23g06.r1
36	108	11.9	662	10	BE307772	BE307772 601097115
37	107	11.8	469	9	AA015563	AA015563 mi61d10.r
38	105.5	11.6	397	9	AA43286	AA43286 zw87h02.s
39	105	11.5	652	10	BB629840	BB629840 BB629840
40	105	11.5	771	13	BI733853	BI733853 603353138
41	104.5	11.5	503	12	BG368728	BG368728 HVSME1002
42	103.5	11.4	691	12	BF682781	BF682781 602117154
43	102	11.2	483	10	BE211563	BE211563 so63d08.y
44	101.5	11.2	639	9	AJ457515	AJ457515 AJ457515
45	100	11.0	970	17	CNS042FU	AL271443 Tetraodon

ALIGNMENTS

RESULT 1  
AI430337  
LOCUS AI430337 524 bp mRNA linear EST 15-MAR-2000  
DEFINITION mf68b10.yl Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA  
clone IMAGE:419419 5', mRNA sequence.  
ACCESSION AI430337  
VERSION AI430337.1 GI:4276173  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 524)  
AUTHORS Maria.M., Hillier.L., Kucaba.T., Martin.J., Beck.C., Wylie.T., Underwood.K., Steptoe.K., Theising.B., Allen.M., Bowers.Y., Person







Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu  
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized hippocampus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)  
Seq primer: M13 Forward  
POLYA=Yes.

# FEATURES

Location/Qualifiers  
1..432  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-CA0-axa-f-12-0-UI"  
/clone\_lib="UI-R-CA0"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; The UI-R-CA0 library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, medulla, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at [ratest.eng.uiowa.edu](http://ratest.eng.uiowa.edu). The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)  
TAG\_LIB=UI-R-CA0  
TAG\_TISSUE=hippocampus  
TAG\_SEQ=GATTG

BASE COUNT 86 a 112 c 133 g 101 t

## Alignment Scores:

Pred. No.: 0.0155 Length: 432  
Score: 126.50 Matches: 29  
Percent Similarity: 52.22% Conservative: 18  
Best Local Similarity: 32.22% Mismatches: 38  
Query Match: 13.90% Indels: 5  
DB: 10 Gaps: 3

US-10-037-591A-2 (1-161) x BE108127 (1-432)

Qy 67 AsnSerArgAlaIleSerProTirpArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86  
Db 383 AACAGAGAGAGCGTCTCTCCCTGGGCTACAGCATCAATACGACCCCGCGCATCCG 324  
Qy 87 GlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySer 106  
Db 323 GAGACATGCTGAGCGCGGTGCTATGTTGGTGGTGGTGAACCCCTTACC----- 270  
Qy 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126  
Db 269 ATGCAGGAGGACCGTAGCATGTGAGCGTGCAGTGTACCGAGGTCCAGTCCGCGCGC 210  
Qy 127 ArgProCysHisGlyGluGlyThrHisLysGlyTyrCysLeuGluArgLeuTyr 146  
Db 209 CGCCTCTGT-----CCGCAACCTCCTCGCGCGGCGCTGCGCGACGCTGTTCATG 156  
Qy 147 Arg---ValSerLeuAlaCysValCysVal 155  
Db 155 GAGACCATCGCTGTGGGTGCACCTGCATC 126

## RESULT 7

BF409208/c 511 bp mRNA linear EST 28-NOV-2000  
LOCUS  
DEFINITION UI-R-BT1-bkn-c-11-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone  
ACCESSION BF409208  
VERSION BF409208.1 GI:11397183

## KEYWORDS

SOURCE  
ORGANISM

EST.  
Norway rat.  
Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

## REFERENCE

1 (bases 1 to 511)

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

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451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized hippocampus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)  
Seq primer: M13 Forward  
POLYA=Yes.

Location/Qualifiers

1..511

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-BT1-bkn-c-11-0-UI"

/clone\_lib="UI-R-BT1"

/dev\_stage="adult"

/lab\_host="DH10B (Life Technologies)"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; The library of UI-R-BT1 is a subtracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at [ratest.eng.uiowa.edu](http://ratest.eng.uiowa.edu). The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)  
TAG\_LIB=UI-R-BT1  
TAG\_TISSUE=hippocampus  
TAG\_SEQ=GATTG

BASE COUNT 97 a 138 c 152 g 124 t

ORIGIN

Alignment Scores:

Pred. No.: 0.0196 Length: 511  
Score: 126.50 Matches: 29  
Percent Similarity: 52.22% Conservative: 18  
Best Local Similarity: 32.22% Mismatches: 38  
Query Match: 13.90% Indels: 5  
DB: 12 Gaps: 3

US-10-037-591A-2 (1-161) x BF409208 (1-511)

Qy 67 AsnSerArgAlaIleSerProTirpArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86  
Db 384 AACAGAGAGAGCGTCTCTCCCTGGGCTACAGCATCAATACGACCCCGCATCCG 325  
Qy 87 GlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySer 106  
Db 324 GAGGACTTGCCTGAGCGCGGTGCTATGTTGGTGGTGGTGAACCCCTTACC----- 271  
Qy 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126

```

Db 270 ATCGAGGAGACGTAGCATGGTGGAGCGTCCAGTGTTCAGCCAGTGCCAGTCCGCGC 211
      |||      |||      |||      |||      |||      |||      |||      |||
QY 127 ArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgLeuTyr 146
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 210 CGCCTCTGT-----CGGCAACCTCTCGCGCGCGCGCTGCCCGCCAGCGTGTGTCTATG 157
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 147 Arg---ValSerLeuAlaCysValCysVal 155
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 156 GAGACCATCGTGTGGTTCACCTGCATC 127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
BQ211497/c
LOCUS BQ211497 533 bp mRNA linear EST 02-MAY-2002
DEFINITION UI-R-DY1-cnq-f-07-0-UI.s1 UI-R-DY1 Rattus norvegicus cDNA clone
ACCESSION BQ211497
VERSION BQ211497.1 GI:20427962
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 533)
          Bonaldo,M.F., Lennon,G. and Soares,M.B.
          Normalization and subtraction: two approaches to facilitate gene
          discovery
          Genome Res. 6 (9), 791-806 (1996)
JOURNAL 97044477
MEDLINE Contact: Soares, MB
COMMENT Program for Rat Gene Discovery and Mapping
          University of Iowa
          451 Eckstein Medical Research Building Iowa City, IA 52242, USA
          Tel: 319 335 8250
          Fax: 319 335 9565
          Email: msoares@blue.weeg.uiowa.edu
          The sequence contained an oligo-dT track that was present in the
          oligonucleotide that was used to prime the synthesis of first
          strand cDNA and therefore this may represent a bonafide poly A
          tail. The sequence tag present in the cDNA between the NotI site
          and the oligo-dT track served to verify it as a clone from the
          normalized cartilage library cDNA Library Preparation: M.B. Soares
          Lab Clone distribution: clones will be available through Research
          Genetics (www.resgen.com)
          Seq primer: M13 Forward
          POLYA=Yes.
          Location/Qualifiers
            1..533
              /organism="Rattus norvegicus"
              /strain="Sprague-Dawley"
              /db_xref="taxon:10116"
              /clone="UI-R-DY1-cnq-f-07-0-UI"
              /clone_lib="UI-R-DY1"
              /tissue_type="Cartilage"
              /dev_stage="Adult"
              /lab_host="DH10B (Life Technologies)"
              /note="Organ: Femur and Tibia; Vector: pT73D-Pac
              (Pharmacia) with a modified polylinker; Site 1: Not I;
              Site 2: Eco RI; UI-R-DY1 is a normalized cDNA library
              containing the following tissue(s): Rat Cartilage from
              Femur and Tibia. The library was constructed according to
              Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
              1996. First strand cDNA synthesis was primed with an
              oligo-dT primer containing a Not I site. Double stranded
              cDNA was ligated to an EcoR I adaptor, digested with Not
              I, and cloned directionally into pT73-Pac vector. The
              oligonucleotide used to prime the synthesis of
              first-strand cDNA contains a library tag sequence that is
              located between the Not I site and the (dT)18 tail. The
              sequence tag for this library is CTATGGACG. The Rat
              cartilage tissue was provided by Dr Jeff Stevens at the
              University of Iowa.

```

```

TAG_LIB=UI-R-DY1
TAG_TISSUE=cartilage
TAG_SEQ=CTATGGACG"
BASE COUNT 103 a 147 c 157 g 125 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 0.0207 Length: 533
Score: 126.50 Matches: 29
Percent Similarity: 52.22% Conservative: 18
Best Local Similarity: 32.22% Mismatches: 38
Query Match: 13.90% Indels: 5
Db: 14 Gaps: 3

US-10-037-591A-2 (1-161) x BQ211497 (1-533)
QY 67 AsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 384 AACAGAGAGAGCGCTGTCTCCCTGGGGCTACAGCATCATCAGCAGCCCGCGCATCCG 325
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 87 GlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySer 106
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 324 GAGCATTGCTGAGCGCGGTGCTATGTTGGGTTCGTGAACCCCTTACC----- 271
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 270 ATGAGGAGGAGCGTAGCATGCTGAGCGTTCAGCGTTCAGCGGCGCGCGC 211
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 ArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgLeuTyr 146
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 210 CGCCTCTGT-----CGCAACCTCTCGCGCGCGCGCTGCCCGCAGCGTGTGTCTATG 157
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 147 Arg---ValSerLeuAlaCysValCysVal 155
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 156 GAGACCATCGTGTGGTTCACCTGCATC 127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
BQ209760/c
LOCUS BQ209760 561 bp mRNA linear EST 02-MAY-2002
DEFINITION UI-R-DZ1-cog-i-01-0-UI.s1 UI-R-DZ1 Rattus norvegicus cDNA clone
          UI-R-DZ1-cog-i-01-0-UI 3', mRNA sequence.
ACCESSION BQ209760
VERSION BQ209760.1 GI:20426225
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 561)
          Bonaldo,M.F., Lennon,G. and Soares,M.B.
          Normalization and subtraction: two approaches to facilitate gene
          discovery
          Genome Res. 6 (9), 791-806 (1996)
JOURNAL 97044477
MEDLINE Contact: Soares, MB
COMMENT Program for Rat Gene Discovery and Mapping
          University of Iowa
          451 Eckstein Medical Research Building Iowa City, IA 52242, USA
          Tel: 319 335 8250
          Fax: 319 335 9565
          Email: msoares@blue.weeg.uiowa.edu
          The sequence contained an oligo-dT track that was present in the
          oligonucleotide that was used to prime the synthesis of first
          strand cDNA and therefore this may represent a bonafide poly A
          tail. The sequence tag present in the cDNA between the NotI site
          and the oligo-dT track served to verify it as a clone from the
          normalized cartilaginous tumor library cDNA Library Preparation:
          M.B. Soares Lab Clone distribution: clones will be available
          through Research Genetics (www.resgen.com)
          Seq primer: M13 Forward
          POLYA=Yes.
          Location/Qualifiers

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FEATURES



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source
1. .561
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-D21-cog-i-01-0-UI"
/clone_lib="UI-R-D21"
/tissue_type="Chondrosarcoma"
/dev_stage="37 days"
/lab_host="DH10B (Life Technologies)"
/notes="Organ: Spine; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site.1: Not 1; Site.2: Eco RI;
UI-R-D21 is a normalized cDNA library containing the
following tissues: Swam Rat Chondrosarcoma. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73D-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CAATCTTGTGA. The Rat cartilaginous tumor tissue was
provided by Dr Jeff Stevens at the University of Iowa.
TAG_LIB=UI-R-D21
TAG_TISSUE=cartilaginous tumor
TAG_SEQ=CAATCTTGTGA"
BASE COUNT 107 a 154 c 173 g 127 t
ORIGIN

Alignment Scores:
Pred. No.: 0.0223 Length: 561
Score: 126.50 Matches: 29
Percent Similarity: 52.22% Conservatve: 18
Best Local Similarity: 32.22% Mismatches: 38
Query Match: 13.90% Indels: 5
DB: 14 Gaps: 3

US-10-037-591A-2 (1-161) x BQ209760 (1-561)
Qy 67 AsnSerArgAlaIleSerProTrrpArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86
Db 384 AACAGAGAGAGCGCTGTCCCTGGGGCTACAGCATCAATCAGACCCAGCGCATCCCG 325
Qy 87 GlnAspLeuTyrHisAlaArgCysLeuSerProHisCysValSerLeuGlnThrGlySer 106
Db 324 GAGACCTGCTGAGCGCGGCTGTGCTATGTTGGGTGGTGAACCCCTTACCC----- 271
Qy 107 HisMetAspProArgGlyAsnSerGluLeuTyrHisAsnGlnThrValPheTyrArg 126
Db 270 ATGCAGGAGGACCGTAGCATGGTGAGCGTGCACGTTCAGCCAGCGTGCAGTGCAGCGC 211
Qy 127 ArgProCysHisGlyGlyGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyr 146
Db 210 CGCCTCTGT-----CCGCAACCTCCTCGCGCGCGCGCTGCGCGCGCGTGTGTCATG 157
Qy 147 Arg---ValSerLeuAlaCysValCysVal 155
Db 156 GAGACCATCGTGTGGGTGCACCTGCATC 127

RESULT 10
BQ604493/c 678 bp mRNA linear EST 24-JUN-2002
LOCUS
DEFINITION MI-P-CPI-nzc-b-11-0-UI.s1 MI-P-CPI Sus scrofa cDNA clone
MI-P-CPI-nzc-b-11-0-UI 3', mRNA sequence.
ACCESSION BQ604493
VERSION BQ604493.1 GI:21551219
KEYWORDS EST.
SOURCE p19.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 678)

```

Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
Contact: Tuggle CK  
Molecular Genetics Laboratory, Department of Animal Science  
Iowa State University  
201 Kildee Hall, Ames, IA 50011-3150, USA  
Tel: 5152944252  
Fax: 5152942401  
Email: cktuggle@iastate.edu  
Tissue Procurement: Dr. Chris Tuggle, Iowa State University  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
The following repetitive elements were found in this cDNA  
sequence: 243-304, >GC-richLow\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA-Yes.

Location/Qualifiers  
1. .678  
/organism="Sus scrofa"  
/strain="crossbreed"  
/db\_xref="taxon:9823"  
/clone="MI-P-CPI-nzc-b-11-0-UI"  
/clone\_lib="MI-P-CPI"  
/lab\_host="DH10B (Life Technologies)"  
/notes="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site.1: Not 1; Site.2: EcoRI; The MI-P-CPI  
library is normalized library derived from the MI-P-CPI  
library, ultimately derived from uterus tissue. For a  
detailed description of the library from which this clone  
was derived, please visit our web site at  
http://pigest.genome.iastate.edu/. The procedure used to  
create this library has been previously described (Bonaldo  
, Lennon and Soares, Genome Research 6: 791-806, 1996)  
TAG\_LIB=MI-P-CPI  
TAG\_TISSUE=uterus  
TAG\_SEQ=AGTCCAATCG"

BASE COUNT 95 a 216 c 224 g 142 t 1 others  
ORIGIN

Alignment Scores:  
Pred. No.: 0.0323 Length: 678  
Score: 126.00 Matches: 34  
Percent Similarity: 44.25% Conservatve: 16  
Best Local Similarity: 30.09% Mismatches: 39  
Query Match: 13.85% Indels: 24  
DB: 14 Gaps: 4

US-10-037-591A-2 (1-161) x BQ604493 (1-678)  
Qy 67 AsnSerArgAlaIleSerProTrrpArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86  
Db 465 AACACAGAGAGCGCTGTACCCCTGGGGCTACAGCATCAACACACACCCCGCATCCCC 406  
Qy 87 GlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySer 106  
Db 405 GCGGACCTGCCGAGCGCGGTGCTGTCTGGGCTGTGTGAACCCCTTACCC----- 352  
Qy 107 HisMetAspProArgGlyAsnSerGluLeuTyrHisAsnGlnThrValPheTyrArg 126  
Db 351 ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCTGTTTCAGCCAGCGTGCCTGCGCGCGC 292  
Qy 127 ArgProCysHisGlyGlyGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyr 146  
Db 291 CGCCTCTGTCCCTGCGCACCGCGCAC-----GGGCCCTGCGCGCGCGGTGTCATG 238  
Qy 147 Arg---ValSerLeuAlaCysValCysVal----- 155  
Db 156 GAGACCATCGTGTGGGTGCACCTGCATC 127

```

Db 237 GAGACATCGCGGGCTGACCTGCTGCTTCTGAGACGCCCTCCCGCGCCCCCAGCC 178
Qy 156 -----ArgProArgVal 159
Db 177 GCGAGCCAGGCGCGGGTGAAGCAGACCTCGGGTC 139

RESULT 11
AI867949/c
LOCUS
DEFINITION
  wb90b08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2312919 3'
  similar to contains Alu repetitive element; mRNA sequence.
ACCESSION
  AI867949
VERSION
  AI867949.1 GI:5540965
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 373)
REFERENCE
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgaps-femail.nih.gov
  Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: M. Bento Soares, Ph.D.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Insert length: 764 Std Error: 0.00
  Seq primer: -400P from Gibco
  High quality sequence stop: 305.
  Location/Qualifiers
    1..373
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:2312919"
    /clone_lib="NCI_CGAP_Pr28"
    /sex="male"
    /dev_stage="adult"
    /lab_host="DH10B"
    /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
    with a modified polylinker; Plasmid DNA from the
    normalized library NCI_CGAP_Pr22 was prepared, and ss
    circles were made in vitro. Following HAP purification,
    this DNA was used as tracer in a subtractive hybridization
    reaction. The driver was PCR-amplified cDNAs from a pool
    of 5,000 clones made from the same library (clonoids
    985608-986759, 1101192-1101959, and 1217928-1220615).
    985608-986759, 1101192-1101959, and 1217928-1220615."
    Subtraction by Bento Soares and M. Fatima Bonaldo.
  BASE COUNT
  ORIGIN
    66 a 109 c 131 g 67 t.

Alignment Scores:
Pred. No.: 0.0158 Length: 373
Score: 125.50 Matches: 30
Percent Similarity: 51.11% Conservative: 16
Best Local Similarity: 33.33% Mismatches: 39
Query Match: 13.79% Indels: 5
DB: 9 Gaps: 3

US-10-037-591A-2 (1-161) x AI867949 (1-373)

Qy 67 AsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86
Db 326 AACAGAGGAGCGCTGTCCTCCCTGGGGCTACAGCATCAACACGACGCCCGGTATCCCC 267
Qy 87 GlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySer 106
  ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

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Db 266 GTGACCTCGCGGAGGACGGTGCCTGTGTGCGCTGTGTGAACCCCTTCACC----- 213
Qy 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126
  :::: ||| :::: ||| :::: |||
Db 212 ATGCAGGAGGAGCGAGCATGTTGCGGGTGTTCACGACGAGTTCCTGTGCGCCGC 153
  :::: ||| :::: ||| :::: |||
Qy 127 ArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyr 146
  ||| ||| ||| ||| ||| ||| ||| |||
Db 152 CGCTCTCGCGCCACCGCCCGCCAC-----GGCCCTTGGCCGACGCGCAGTCATG 99
  :::: ||| :::: ||| :::: |||
Qy 147 Arg---ValSerLeuAlaCysValCysVal 155
  :::: ||| :::: ||| :::: |||
Db 98 GAGACCATCGCTGTGGGCTGCACCTGCATC 69

RESULT 12
AI375735/c
LOCUS
DEFINITION
  t664c02.x1 Soares_total_fetus_Nb2HF8.9w Homo sapiens cDNA clone
  IMAGE:2048834 3' similar to contains MER22.b1 TAR1 repetitive
  element; mRNA sequence.
ACCESSION
  AI375735
VERSION
  AI375735.1 GI:4175725
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 405)
REFERENCE
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgaps-remail.nih.gov
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Insert length: 750 Std Error: 0.00
  Seq primer: -400P from Gibco
  High quality sequence stop: 403.
  Location/Qualifiers
    1..405
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:2048834"
    /clone_lib="Soares_total_fetus_Nb2HF8.9w"
    /dev_stage="8-9 weeks"
    /lab_host="DH10B"
    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
    polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
    was prepared from mRNA obtained from pooled 8-9 week
    (total) fetus material with a Not I - oligo(dT) primer [5'
    TGTACCAATCTGAAGTGGAGCGCGCTTAATTTTATTTTATTTT 3'].
    Double-stranded cDNA was ligated to Eco RI adaptors
    (Pharmacia), digested with Not I and cloned into the Not I
    and Eco RI sites of the modified pT7T3 vector. Library
    went through one round of normalization, and was
    constructed by Bento Soares and M. Fatima Bonaldo.
  BASE COUNT
  ORIGIN
    73 a 114 c 133 g 85 t

Alignment Scores:
Pred. No.: 0.0177 Length: 405
Score: 125.50 Matches: 30
Percent Similarity: 51.11% Conservative: 16
Best Local Similarity: 33.33% Mismatches: 39
Query Match: 13.79% Indels: 5
DB: 9 Gaps: 3

US-10-037-591A-2 (1-161) x AI375735 (1-405)

Qy 67 AsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86
Db 367 AACAGAGGAGCGCTGTCCTCCCTGGGGCTACAGCATCAACACGACGCCCGGTATCCCC 308
  ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

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QY 87 GlnAspLeuTyrHisAlaArgCysProHisCysValSerLeuGlnThrGlySer 106
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 GTGGACCTGCCGAGCAGCGTCTGCTCGGCTGTGTGAACCCCTTACC----- 254
QY 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126
    :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 253 ATGCAGGAGGACCGCAGCAGTGTGAGCGTGGCGGTGTTTCAGCCAGGTTCTCTGCGCGCG 194
QY 127 ArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgLeuTyr 146
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 193 CGCCTCTCCCGCCACCACCGCCGCACA-----GGCCTTGCCGCGCAGCGCAGTCATG 140
QY 147 Arg---ValSerLeuAlaCysValCysVal 155
    :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 GAGACCATCGTGTGGGTGCACCTGCATC 110

RESULT 13
AI370793/c
LOCUS
DEFINITION ta58a04.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:2048238 3', mRNA sequence.
ACCESSION AI370793
VERSION AI370793.1 GI:4149546
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 467)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 794 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 439.
Location/Qualifiers
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/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer
[5'
TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 83 a 135 c 144 g 105 t
ORIGIN

Alignment Scores:
Pred. No.: 0.0216 Length: 467
Score: 125.50 Matches: 30
Percent Similarity: 51.11% Conservative: 16
Best Local Similarity: 33.33% Mismatches: 39
Query Match: 13.79% Indels: 5
DB: 9 Gaps: 3

US-10-037-591A-2 (1-161) x AI370793 (1-467)

QY 67 AsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86

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Db 369 ACAAGAGAGCGCTGTCTCCTGGGCTACAGCATCAACCCAGCCGCTATCCCC 310
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 309 GTGGACCTGCCGAGCAGCGTCTGCTCGGCTGTGTGAACCCCTTACC----- 256
QY 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126
    :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 255 ATGCAGGAGGACCGCAGCAGTGTGAGCGTGGCGGTGTTTCAGCCAGGTTCTCTGCGCGCG 196
QY 127 ArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgLeuTyr 146
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 195 CGCCTCTCCCGCCACCACCGCCGCACA-----GGCCTTGCCGCGCAGCGCAGTCATG 142
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RESULT 14
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LOCUS
DEFINITION af37c02.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:1033826 3', mRNA sequence.
ACCESSION AA780147
VERSION AA780147.1 GI:2839478
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 468)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
CONTACT: Wilson RK
JOURNAL Washington University School of Medicine
COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 392.
Location/Qualifiers
1..468
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1033826"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer
[5'
TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 82 a 135 c 147 g 104 t
ORIGIN

Alignment Scores:
Pred. No.: 0.0216 Length: 468
Score: 125.50 Matches: 30
Percent Similarity: 51.11% Conservative: 16

```



GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003: Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 01:06:09 ; Search time 1066 Seconds  
(without alignments)  
9784.140 Million cell updates/sec

Title: US-10-037-591A-1

Perfect score: 644

Sequence: 1 ctcaagtcactccctaaaaa.....ggcccggtgtagggctag 644

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpi:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	296.4	46.0	524	9	AI430337
2	249.6	38.8	420	14	W88186
3	229	35.6	553	13	BM540145
4	145.4	22.6	344	12	BG609875
5	96.6	15.0	480	13	BM124559
6	96.6	15.0	549	14	BQ554452

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C	8	47	7.3	997	17	CNS006DN	AL065132 Drosophila
C	9	43.8	6.8	868	12	BG821981	BG821981 602726077
C	10	43.2	6.7	925	17	CNS0091P	AL053013 Drosophila
C	11	43	6.7	568	14	BQ574994	BQ574994 UI-H-E21-
C	12	42.8	6.6	440	14	BQ779177	BQ779177 946117505
C	13	42.4	6.6	839	17	CNS004NB	AL054280 Drosophila
C	14	42.2	6.6	460	10	BE357122	BE357122 DGL_146_B
C	15	42.2	6.6	486	9	AI388531	AI388531 GH19472.5
C	16	42.2	6.6	586	10	BE357121	BE357121 DGL_146_B
C	17	42.2	6.6	588	13	BM055698	BM055698 i88h04.x
C	18	42.2	6.6	533	13	BM330143	BM330143 PIC3_47_F
C	19	42.2	6.6	652	10	BE362682	BE362682 DGL_88_H0
C	20	41.6	6.5	441	9	AI064196	AI064196 GH04480.5
C	21	41.4	6.4	373	9	AI867949	AI867949 w900008.x
C	22	41.4	6.4	396	9	AA680405	AA680405 z138h02.s
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C	26	41.2	6.4	463	13	BM381881	BM381881 MEST541-D
C	27	41.2	6.4	488	9	AI854942	AI854942 605094E01
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C	30	41.2	6.4	556	10	AW787571	AW787571 945011B07
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C	35	41.2	6.4	586	10	BE511474	BE511474 946061B04
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C	44	40.6	6.3	553	9	AI323984	AI323984 mb22a01.x
C	45	40.6	6.3	602	13	BM053185	BM053185 id66d06.x

#### ALIGNMENTS

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mf68b10.y1 Soares mouse embryo NMEL13.5 14.5 Mus musculus CDNA  
Clone IMAGE:419419 5', mRNA sequence.

AI430337  
AI430337.1 GI:4276173

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

ORGANISM

house mouse.  
Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 524)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person,  
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter,  
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.

REFERENCE

AUTHORS

TITLE  
JOURNAL

COMMENT

Unpublished (1999)

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

This read is a RESEQUENCE of a previously sequenced mouse clone



Ddb	242	CTCCACATGGACCGCTGGGCAACTCGTCCCACTTTACACACACAGCAGCGTCTTCTTA	301
Qy	533	CGCGGGCCATGCCATGGCGAGAGGGCACCCACCAAGGCTACTCCTGGAGCGCAGGCT	592
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DEFINITION	hb18f07.g1 Canis cDNAs from testes cells Canis familiaris cDNA	553 bp	linear
ACCESSION	BH540145		EST 20-FEB-2002
VERSION	BH540145.1	GI:18822687	
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SOURCE	dog.		
ORGANISM	Canis familiaris		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
AUTHORS	1 (bases 1 to 553) O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Baliya,V., Cunniss D., Dedhia,N.N., de la Bastide,M., Katzenberger,F., King,L., Kirchoff,K.A., Miller,B., Muller,S., Nascimento,L.U., Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T., Preston,R. and Hannon,G.J.		
TITLE	Expressed sequence tags from Canis familiaris (dog) (2002)		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mcombie@cshl.org Plate: hb18 row: f column: 07 Seq primer: -21M13UnivRev High quality sequence stop: 553. Location/Qualifiers		
FEATURES	1..553 /organism="Canis familiaris" /db_xref="taxon:9615" /clone="hb18f07" /clone_lib="Canis cDNAs from testes cells" /tissue_type="testes" /note="Vector: Lambda zap II; The library was produced by Greg Hannon and Raymond Preston (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using stratagene zap cDNA synthesis kit. It was made from dog testes. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries." 138 a 171 c 143 g 101 t		
BASE COUNT			
ORIGIN			
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Best Local Similarity	74.68;	Pred. No. le-44;	
Matches	341; Conservative	0; Mismatches	85; Indels 31; Gaps 3;
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Ddb	164	TAAACACGAGACACCGGAGCTGTCTCCAGTCAGCCTGCC	217
Qy	126	GCCCCATTGTGATGTGATGTGCGAGTGCACCGCATGTACACAGGTGTTGCAATCTTGCA	185
Ddb	218	GTAGCAC-CGTGGCTGGCGCAGCATCAGCATGATCAGGTGATCGTGTCTCTTGTA	276









XX PR 11-JAN-1999; 99US-0229402.  
 XX PA (SCHE ) SCHERING CORP.  
 XX PI Gorman DM, Bazan JF, Kastelein RA;  
 XX DR WPI; 2000-476060/41.  
 XX DR N-PSDB; AAA59158.  
 XX PT New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
 XX PT interleukin-171 (IL-171), useful for recombinant production of IL-171  
 XX PT which can be used for treating conditions associated with abnormal  
 XX PT physiology or development -  
 XX PS Disclosure; Page 19; ilipp; English.  
 XX CC The present sequence represents an interleukin (IL)-174 polypeptide.  
 XX CC It is a mammalian homologue of the cytokine designated CTLA-8 (also  
 XX CC referred to as IL-17). The specification also describes homologues  
 XX CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
 XX CC sequence encoding IL-171 is useful for identifying genes, mRNA and  
 XX CC cDNA molecules which code for related or homologous proteins. The  
 XX CC IL-171 protein, antibodies against IL-171, and compounds which have  
 XX CC binding affinity to IL-171 are useful in treatment of conditions  
 XX CC associated with abnormal physiology or development, including abnormal  
 XX CC proliferation, e.g. cancerous conditions, or degenerative conditions.  
 XX CC The IL-171 protein can be used in kits and assay methods for identifying  
 XX CC compounds that selectively bind to IL-171.  
 XX CC  
 XX CC Sequence 161 AA;  
 XX CC  
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 XX CC Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
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 XX AC AAE18120 standard; Protein; 161 AA.  
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 XX AC AAE18120;  
 XX XX  
 XX DT 07-MAY-2002 (first entry)  
 XX XX  
 XX DE Human Interleukin-17 like (IL-17L) protein.  
 XX KW Human; interleukin-17 like; IL-17L; immune system dysfunction; diabetes;  
 XX KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;  
 XX KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;  
 XX KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;  
 XX KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
 XX KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
 XX KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
 XX KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
 XX KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
 XX KW cancer.  
 XX XX  
 XX OS Homo sapiens.  
 XX XX  
 XX FH Key Location/Qualifiers

Peptide 1..16  
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 Protein 17..161  
 /label= Mature\_IL\_17L\_protein  
 WO200208285-A2.  
 31-JAN-2002.  
 21-JUN-2001; 2001WO-US19861.  
 22-JUN-2000; 2000US-213125P.  
 02-FEB-2001; 2001US-266159P.  
 16-MAR-2001; 2001US-0810384.  
 (AMGE-) AMGEN INC.  
 Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HO, Jing S;  
 WPI: 2002-155217/20.  
 N-PSDB; AAD28771.  
 Nucleic acid molecules encoding Interleukin 17 (IL-17) - like  
 polypeptides useful in the treatment, prevention and diagnosis of  
 diseases e.g. cancer  
 Claim 13; Fig 1; 242pp; English.  
 The invention relates to nucleic acid molecules encoding Interleukin 17  
 (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
 of IL-17 protein in an animal. The IL-17 protein is useful for treating,  
 preventing or ameliorating a disease, such as immune system dysfunction  
 (rheumatoid arthritis, osteoarthritis, diabetes, inflammatory bowel  
 autoimmune multiple sclerosis, lupus, diabetes, inflammatory bowel  
 disease, transplant rejection, graft vs. host disease); infections (HIV,  
 hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,  
 sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
 (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin  
 (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
 (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy  
 atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma  
 leukaemia); reproductive (infertility, miscarriage, endometriosis), eye  
 (blindness, retinal neuropathy) and treatment of diseases involving  
 inflammation. The present sequence is human Interleukin-17 like (IL-17L)  
 protein.  
 Sequence 161 AA;  
 Query Match 100.0%; Score 910; DB 23; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MYQVAFAMVGMTHYTHSWPSCCPKSGQDTSELLRWSTVPVPPLEPARNHPESCRA 60  
 DB 1 MYQVAFAMVGMTHYTHSWPSCCPKSGQDTSELLRWSTVPVPPLEPARNHPESCRA 60  
 QY 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLCPHCVSLQTGSHMDPRGNSELYHN 120  
 DB 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLCPHCVSLQTGSHMDPRGNSELYHN 120  
 QY 121 QTVFYRRPCHGKGTGKGYCLERRLYRSLACVVCVRPVNG 161  
 DB 121 QTVFYRRPCHGKGTGKGYCLERRLYRSLACVVCVRPVNG 161  
 RESULT 4  
 ID AAM52691  
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 XX AAM52691;  
 XX XX  
 XX DT 26-FEB-2002 (first entry)  
 XX XX



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XX  
ZNY 00076/T0070M N3

PD	25-OCT-2001.
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XX	
PF	17-APR-2001; 2001WO-US12493.
XX	
XX	
PR	18-APR-2000; 2000US-198488P.
XX	
XX	
PA	(SCHE ) SCHERING CORP.
XX	
PI	Hurst SD, Zurawski SM, Rennick DM;
XX	
XX	
WPI	2002-034343/04.
DR	
D-PSDB	AAW526G1

Disclosure; Page 26-27; 29pp; English.

The invention relates to methods of directing an immune response in a mammal by the administration of an agonist or antagonist of the cytokine interleukin 174 (IL-174). Administration of an IL-174 agonist directs the immune response towards a Th2 response, stimulates an innate immune response, augments the inflammatory response from epithelial or fibroblast cells, induces gut cell growth, promotes extramedullary haematopoiesis, or augments an antibody response in serum and faecal material, while administration of an IL-174 antagonist directs the immune response away from a Th2 type response, and prevents inflammation or granuloma formation. IL-174 agonists may be used to treat autoimmune conditions (particularly multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, diabetes or psoriasis), a response to an infectious agent, or inflammatory conditions such as Crohn's disease, ulcerative colitis, pancreatitis, or hepatitis. IL-174 antagonists may be used to treat inflammatory, allergic or Th2-mediated conditions (e.g., systemic anaphylactic response, skin hypersensitivity response, dermatitis, asthma, fibrosis, or eosinophilic gastritis). The present sequence represents DNA encoding human IL-174.

Sequence 504 BP: 98 A: 165 C: 148 G: 93 T: 0 other:

Alignment Score:

Pred. No.:	3.01e-74	Length:	504
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Score: 910.00

Percent Similarity: 100.00%  
Conservative: 0

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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Conservative: 0

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Query Match:	100.00%	Indels:	0
DB:	2A	Gaps:	0

DB:	24	Gaps:	0
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US-10-037-591A-2 (1-161) x ABA02393 (1-504)

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19 ATGTACCAAGTGGTTGGTTCATTCTTTGGCAATGGTCAATGGGAACCCACACCTTACAGCCACTGG 78

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Ov	21	ProSerCueDroSerIValClValAlaThrMetSerClValLysIleLeuThrMetSerMetb

Qy 21 ProSerCysCysProSerLysGlyGlnaspThrSerGluGluLeuLeuargTrpSerThr 40

Db 79 CCCAGCTGCTGCCCCCAGCAAGGGCGACACCTCTGAGGAGCTCTGAGGTGGAGCACT 138

QY 41 ValProValProProLeuGluProAlaArgPro

Db 139 GTGCCTGTGCCTCCCTAGAGCTGTAGGCCCAACCGCCACCCAGAGTCTGTAGGGCC 198

QY 61 SerGluAspGlyProIleuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArg 80

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VERSION AX164145.1 GI:14545087  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 1320)  
AUTHORS Fong, S., Goddard, A., Godowski, P. J., Grimaldi, C. J., Gurney, A. L., Hillan, K. J., Tumas, D., Watanabe, C. K., Wood, W. I., and Zhang, Z.  
TITLE Compositions and methods for the treatment of immune related diseases  
JOURNAL Patent: WO 0140465-A 17 07-JUN-2001;  
Genentech, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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VERSION AX180768.1 GI:15132618  
KEYWORDS human.  
SOURCE Homo sapiens  
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REFERENCE 1 (bases 1 to 1320)  
AUTHORS Chen, J., Filvaroff, E., Fong, S., Goddard, A., Godowski, P. J., Grimaldi, C. J., Gurney, A. L., Li, H., Hillan, K. J., Tumas, D., van Lookeren, M., Vandlen, R. L., Watanabe, C. K., Williams, P. M., Wood, W. I., and Yansura, D. G.

TITLE Il-17 and il-17r homologous polypeptides and therapeutic uses thereof  
JOURNAL Patent: WO 0146420-A 5 28-JUN-2001;  
Genentech, Inc. (US)  
FEATURES  
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BASE COUNT 280 a 353 c 384 g 303 t  
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Best Local Similarity 99.8%; Pred. No. 6.6e-108;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 165 CAGGTGTTGATCTTGGCAATGGTCTAGGAAACCCACACACCTACAGCCACTGCCCCAGC 224  
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QY 285 GTGCCTCCCTAGAGCTGCTAGGAAACCCACACACCTACAGCCACTGCCCCAGC 344  
Db 433 GTGCCTCCCTAGAGCTGCTAGGAAACCCACACACCTACAGCCACTGCCCCAGC 492  
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Db 493 GATGGACCCCTCAACAGCAGGCGCATCTCCCTCGGAGATATGATGGACAGAGACTTG 552  
QY 405 AACCGGCTCCCGAGGACCTGTACACGCGCGCTGCTGCGCGCAGCTGCTGCGCGCAGCTA 464  
Db 553 AACCGGCTCCCGAGGACCTGTACACGCGCGCTGCTGCGCGCAGCTGCTGCGCGCAGCTA 612  
QY 465 CAGCAGGCTCCCGAGGACCTGTACACGCGCGCTGCTGCGCGCAGCTGCTGCGCGCAGCT 524  
Db 613 CAGCAGGCTCCCGAGGACCTGTACACGCGCGCTGCTGCGCGCAGCTGCTGCGCGCAGCT 672  
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Db 673 GTCCTTACCGCGCGCATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 732  
QY 585 CGCAGGCTGACCGTGTTCCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 644  
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DEFINITION AF305200  
ACCESSION AF305200  
VERSION AF305200.1 GI:11878209  
KEYWORDS Homo sapiens.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 1335)  
AUTHORS Lee, J., Ho, W.-H., Maruoka, M., Corpuz, R. T., Baldwin, D. T., Foster, J. S., Goddard, A. D., Yansura, D. G., Vandlen, R. L., Wood, W. I., and Gurney, A. L.  
TITLE IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog IL-17Rhl  
JOURNAL J. Biol. Chem. 276 (2), 1660-1664 (2001)  
MEDLINE 21125711  
PUBMED 11058597  
REFERENCE 2 (bases 1 to 1335)  
AUTHORS Lee, J., Ho, W.-H., Maruoka, M., Corpuz, R. T., Baldwin, D., Foster, J. S., Goddard, A. D., Yansura, D. G., Vandlen, R. L., Wood, W. I., and Gurney, A. L.  
TITLE Direct Submission  
JOURNAL Submitted (12-SEP-2000) Molecular Biology, Genentech, 1 DNA Way,

